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(54) Title: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA LIBRARY. APPLICATION TO THE DETECTION OF MYCOBACTERIA

(57) Abstract

The present invention is directed to a method for isolating a polynucleotide of interest that is present or is expressed in a genome of a first mycobacterium strain and that is absent or altered in a genome of a second mycobacterium strain which is different from the first mycobacterium strain using a bacterial artificial chromosome (BAC) vector. The invention further relates to a polynucleotide isolated by this method and recombinant BAC vector used in this method. In addition the present invention comprises method and kit for detecting the presence of a mycobacteria in a biological sample.

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**A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA LIBRARY. APPLICATION TO THE DETECTION OF MYCOBACTERIA.**

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**I. Background of the invention**

The present invention pertains to a method for isolating a polynucleotide of interest that is present in the genome of a mycobacterium strain and/or is expressed by said mycobacterium strain and that is absent or altered in the 10 genome of a different mycobacterium strain and/or is not expressed in said different mycobacterium strain, said method comprising the use of at least one clone belonging to a genomic DNA library of a given mycobacterium strain, said DNA library being cloned in a bacterial artificial chromosome (BAC). The invention concerns also polynucleotides identified by the above method, as well 15 as detection methods for mycobacteria, particularly *Mycobacterium tuberculosis*, and kits using said polynucleotides as primers or probes. Finally, the invention deals with BAC-based mycobacterium DNA libraries used in the method according to the invention and particularly BAC-based *Mycobacterium tuberculosis* and *Mycobacterium bovis* BCG DNA libraries.

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Radical measures are required to prevent the grim predictions of the World Health Organisation for the evolution of the global tuberculosis epidemic in the next century becoming a tragic reality. The powerful combination of genomics and bioinformatics is providing a wealth of information about the etiologic agent, *Mycobacterium tuberculosis*, that will facilitate the conception and development 25 of new therapies. The start point for genome sequencing was the integrated map of the 4.4 Mb circular chromosome of the widely-used, virulent reference strain, *M. tuberculosis* H37Rv and appropriate cosmids were subjected to systematic shotgun sequence analysis at the Sanger Centre.

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Cosmid clones (Balasubramanian et al., 1996; Pavelka et al., 1996) have played a crucial role in the *M. tuberculosis* H37Rv genome sequencing project. However, problems such as under-representation of certain regions of the chromosome, unstable inserts and the relatively small insert size complicated the 35 production of a comprehensive set of canonical cosmids representing the entire genome.

## II. Summary of the invention

In order to avoid the numerous technical constraints encountered in the state of the art, as described hereabove, when using genomic mycobacterial DNA libraries constructed in cosmid clones, the inventors have attempted to realize 5 genomic mycobacterial DNA libraries in an alternative type of vectors, namely Bacterial Artificial Chromosome (BAC) vectors.

The success of this approach depended on whether the resulting BAC clones could maintain large mycobacterial DNA inserts. There are various reports 10 describing the successful construction of a BAC library for eucaryotic organisms (Cai et al., 1995; Kim et al., 1996; Misumi et al., 1997; Woo et al., 1994; Zimmer et al., 1997) where inserts up to 725 kb (Zimmer et al., 1997) were cloned and stably maintained in the *E. coli* host strain.

Here, it is shown that, surprisingly, the BAC system can also be used for 15 mycobacterial DNA, as 70% of the clones contained inserts in the size of 25 to 104 kb.

This is the first time that bacterial, and specifically mycobacterial, DNA is cloned in such BAC vectors.

In an attempt to obtain complete coverage of the genome with a minimal 20 overlapping set of clones, a Bacterial Artificial Chromosome (BAC) library of *M. tuberculosis* was constructed, using the vector pBeloBAC11 (Kim et al., 1996) which combines a simple phenotypic screen for recombinant clones with the stable propagation of large inserts (Shizuya et al., 1992). The BAC cloning system is based on the *E. coli* F-factor, whose replication is strictly controlled and thus ensures stable maintenance of large constructs (Willets et al., 1987). 25 BACs have been widely used for cloning of DNA from various eucaryotic species (Cai et al., 1995; Kim et al., 1996; Misumi et al., 1997; Woo et al., 1994; Zimmer et al., 1997). In contrast, to our knowledge this report describes the first attempt to use the BAC system for cloning bacterial DNA.

A central advantage of the BAC cloning system over cosmid vectors used 30 in prior art is that the F-plasmid is present in only one or a maximum of two copies per cell, reducing the potential for recombination between DNA fragments and, more importantly, avoiding the lethal overexpression of cloned bacterial genes. However, the presence of the BAC as just a single copy means that plasmid DNA has to be extracted from a large volume of culture to obtain

sufficient DNA for sequencing and it is described here in the examples a simplified protocol to achieve this.

Further, the stability and fidelity of maintenance of the clones in the BAC library represent ideal characteristics for the identification of genomic differences 5 possibly responsible for phenotypic variations in different mycobacterial species.

As it will be shown herein, BACs can be allied with conventional hybridization techniques for refined analyses of genomes and transcriptional activity from different mycobacterial species.

Having established a reliable procedure to screen for genomic 10 polymorphisms, it is now possible to conduct these comparisons on a more systematic basis than in prior art using representative BACs throughout the chromosome and genomic DNA from a variety of mycobacterial species.

As another approach to display genomic polymorphisms, the inventors 15 have also started to use selected H37Rv BACs for "molecular combing" experiments in combination with fluorescent *in situ* hybridization (Bensimon et al., 1994; Michalet et al., 1997). With such techniques the one skilled in the art is enabled to explore the genome of mycobacteria in general and of *M. tuberculosis* in particular for further polymorphic regions.

The availability of BAC-based genomic mycobacterial DNA libraries 20 constructed by the inventors have allowed them to design methods and means both useful to identify genomic regions of interest of pathogenic mycobacteria, such as *Mycobacterium tuberculosis*, that have no counterpart in the corresponding non-pathogenic strains, such as *Mycobacterium bovis* BCG, and useful to detect the presence of polynucleotides belonging to a specific 25 mycobacterium strain in a biological sample.

By a biological sample according to the present invention, it is notably intended a biological fluid, such as plasma, blood, urine or saliva, or a tissue, such as a biopsy.

Thus, a first object of the invention consists of a method for isolating a 30 polynucleotide of interest that is present in the genome of a mycobacterium strain and/or is expressed by said mycobacterium strain and that is absent or altered in the genome of a different mycobacterium strain and/or is not expressed in said different mycobacterium strain, said method comprising the use of at least one clone belonging to a genomic DNA library of a given mycobacterium strain, 35 said DNA library being cloned in a bacterial artificial chromosome (BAC).

The invention is also directed to a polynucleotide of interest that has been isolated according to the above method and in particular a polynucleotide containing one or several Open Reading Frames (ORFs), for example ORFs encoding either a polypeptide involved in the pathogenicity of a mycobacterium strain or ORFs encoding Polymorphic Glycine Rich Sequences (PGRS).

Such polynucleotides of interest may serve as probes or primers in order to detect the presence of a specific mycobacterium strain in a biological sample or to detect the expression of specific genes in a particular mycobacterial strain of interest.

10 The BAC-based genomic mycobacterial DNA libraries generated by the present inventors are also part of the invention, as well as each of the recombinant BAC clones and the DNA insert contained in each of said recombinant BAC clones.

15 The invention also pertains to methods and kits for detecting a specific mycobacterium in a biological sample using either at least one recombinant BAC clone or at least one polynucleotide according to the invention, as well as to methods and kits to detect the expression of one or several specific genes of a given mycobacterial strain present in a biological sample.

20 **III. Brief description of the Figures.**

In order to better understand the present invention, reference will be made to the appended figures which depicted specific embodiments to which the present invention is in no case limited in scope with.

25 **Figures 1A and 1B :** PCR-screening for unique BAC clones with specific primers for 2 selected genomic regions of the H37Rv chromosome, using 21 pools representing 2016 BACs (Figure 1A) and sets of 20 subpools from selected positive pools (Figure 1B).

30 **Figure 2 :** Pulsed-field gel electrophoresis gel of *Dra*I- cleaved BAC clones used for estimating the insert sizes of BACs.

35 **Figure 3 :** Minimal overlapping BAC map of *M. tuberculosis* H37Rv superimposed on the integrated physical and genetic map established by Philipp et al. (18). Y- and I- numbers show pYUB328 (2) and pYUB412 (16) cosmids which were shotgun sequenced during the H37Rv genome sequencing project. Y- cosmids marked with \* were shown in the integrated physical and genetic map

(18). Rv numbers show the position of representative BAC clones relative to sequenced Y- and I- clones. Squared Rv numbers show BACs which were shotgun sequenced at the Sanger Centre.

5 **Figures 4A and 4B :** Ethidium bromide stained gel (Figure 4A) and corresponding Southern blot (Figure 4B) of *Eco*RI and *Pvu*II digested Rv58 DNA hybridized with <sup>32</sup>P labeled genomic DNA preparations from *M. tuberculosis* H37Rv, *M. bovis* ATCC 19210 and *M. bovis* BCG Pasteur.

10 **Figure 5 :** Organisation of the ORFs in the 12.7 kb genomic region present in *M. tuberculosis* H37Rv but not present in *M. bovis* ATCC 19210 and *M. bovis* BCG Pasteur. Arrows show the direction of transcription of the putative genes. Positions of *Eco*RI and *Pvu*II restriction sites are shown. Vertical dashes represent stop codons. The 11 ORFs correspond to the ORFs MTCY277.28 to MTCY277.38 / accession number Z79701 -EMBL Nucleotide Sequence Data Library. The junction sequences flanking the polymorphic region are shown.

15 **Figure 6 :** Variation in the C-terminal part of a PE-PGRS open reading frame in *M. tuberculosis* strain H37Rv relative to *M. bovis* BCG strain Pasteur.

The numbers on the right side of the Figure denote the position of the end nucleotides, taking as the reference the *M. tuberculosis* genome.

20 **Figure 7 :** Polynucleotide sequence next to the HindIII cloning site in the BAC vector pBeloBAC11 (Kim et al., 1996) used to clone the inserts of the BAC-based myobacterial genomic DNA library according to the invention.

NotI : location of the NotI restriction sites.

Primer T7-BAC1 : nucleotide region recognized by the T7-BAC1 primer shown in Table 1.

25 T7 promoter : location of the T7 promoter region on the pBeloBac11 vector.

Primer T7-Belo2 : nucleotide region recognized by the T7-Belo2 primer shown in Table 1.

Hind III : the HindIII cloning site used to clone the genomic inserts in the pBeloBAC11 vector.

30 SP6-Mid primer : nucleotide region recognized by the SP6 Mid primer shown in Table 1.

SP6-BAC1 primer : nucleotide region recognized by the SP6 BAC1 primer shown in Table 1.

SP6 promoter : location of the SP6 promoter region on the pBeloBac11 vector.

#### IV. Detailed description of the preferred embodiments.

As already mentioned hereinbefore, the present invention is directed to a method for isolating a polynucleotide of interest that is present in the genome of a mycobacterium strain and/or is expressed by said mycobacterium strain and that is absent or altered in the genome of a different mycobacterium strain and/or is not expressed in said different mycobacterium strain, said method comprising the use of at least one clone belonging to a genomic DNA library of a given mycobacterium strain, said DNA library being cloned in a bacterial artificial chromosome (BAC) type vector.

For this purpose, the inventors have constructed several BAC-based mycobacterial genomic DNA libraries that may be used in order to perform the above described method.

Because it is the first time that mycobacterial genomic DNA has been successfully cloned in BAC type vectors, and because these DNA libraries are then novel and nonobvious, an object of the present invention consists in a myobacterial genomic DNA library cloned in such a BAC type vector.

As an illustrative example, a BAC-based DNA library of *Mycobacterium tuberculosis* has been realized. Forty-seven cosmids chosen from the integrated map of the 4.4 Mb circular chromosome (Philipp et al., 1996a) were shotgun-sequenced during the initial phase of the H37Rv genome sequence project. The sequences of these clones were used as landmarks in the construction of a minimally overlapping BAC map. Comparison of the sequence data from the termini of 420 BAC clones allowed us to establish a minimal overlapping BAC map and to fill in the existing gaps between the sequence of cosmids. As well as using the BAC library for genomic mapping and sequencing, we also tested the system in comparative genomic experiments in order to uncover differences between two closely related mycobacterial species. As shown in a previous study (Philipp et al., 1996b), *M. tuberculosis*, *M. bovis* and *M. bovis* BCG, specifically BCG Pasteur strain, exhibit a high level of global genomic conservation, but certain polymorphic regions were also detected. Therefore, it was of great interest to find a reliable, easy and rapid way to exactly localize polymorphic regions in mycobacterial genomes using selected BAC clones. This approach was validated by determining the exact size and location of the polymorphisms in the genomic region of *Dra*I fragment Z4 (Philipp et al., 1996b), taking advantage of the availability of an appropriate BAC clone covering the polymorphic region and

the H37Rv genome sequence data. This region is located approximately 1.7 Mb from the origin of replication.

The Bacterial Artificial Chromosome (BAC) cloning system is capable of stably propagating large, complex DNA inserts in *Escherichia coli*. As part of the 5 *Mycobacterium tuberculosis* H37Rv genome sequencing project, a BAC library was constructed in the pBeloBAC11 vector and used for genome mapping, confirmation of sequence assembly, and sequencing. The library contains about 10 5000 BAC clones, with inserts ranging in size from 25 to 104 kb, representing theoretically a 70 fold coverage of the *M. tuberculosis* genome (4.4 Mb). A total of 840 sequences from the T7 and SP6 termini of 420 BACs were determined and 15 compared to those of a partial genomic database. These sequences showed excellent correlation between the estimated sizes and positions of the BAC clones and the sizes and positions of previously sequenced cosmids and the resulting contigs. Many BAC clones represent linking clones between sequenced cosmids, 20 allowing full coverage of the H37Rv chromosome, and they are now being shotgun-sequenced in the framework of the H37Rv sequencing project. Also, no chimeric, deleted or rearranged BAC clones were detected, which was of major 25 importance for the correct mapping and assembly of the H37Rv sequence. The minimal overlapping set contains 68 unique BAC clones and spans the whole H37Rv chromosome with the exception of a single gap of ~ 150 kb. As a post-genomic application, the canonical BAC set was used in a comparative study to reveal chromosomal polymorphisms between *M. tuberculosis*, *M. bovis* and *M. bovis* BCG Pasteur, and a novel 12.7 kb segment present in *M. tuberculosis* but 30 absent from *M. bovis* and *M. bovis* BCG was characterized. This region contains a set of genes whose products show low similarity to proteins involved in polysaccharide biosynthesis. The H37Rv BAC library therefore provides the one skilled in the art with a powerful tool both for the generation and confirmation of sequence data as well as for comparative genomics and a plurality of post-genomic applications.

35 The above described BAC-based *Mycobacterium tuberculosis* genomic DNA library is part of the present invention and has been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on November 19, 1997 under the accession number I-1945.

Another BAC-based DNA library has been constructed with the genomic 35 DNA of *Mycobacterium bovis* BCG, Pasteur strain, and said DNA library has

been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on XX XX, 1998 under the accession number I-XXXX.

Thus, as a specific embodiment of the above described method for isolating a polynucleotide of interest said method makes use of at least one BAC-based DNA library that has been constructed from the genomic DNA of *Mycobacterium tuberculosis*, more specifically of the H37Rv strain and particularly of the DNA library deposited in the accession number I-1945.

In another specific embodiment of the above described method for isolating a polynucleotide of interest said method makes use of at least one BAC-based DNA library that has been constructed from the genomic DNA of *Mycobacterium bovis* BCG, more specifically of the Pasteur strain and particularly of the DNA library deposited in the accession number I-XXXX.

In more details, the method according to the invention for isolating a polynucleotide of interest may comprise the following steps :

- 15 a) isolating at least one polynucleotide contained in a clone of a BAC-based DNA library of mycobacterial origin;
- b) isolating :
  - at least one genomic or cDNA polynucleotide from a mycobacterium, said mycobacterium belonging to a strain different from the strain used to construct the BAC-based DNA library of step a); or alternatively
  - at least one polynucleotide contained in a clone of a BAC-based DNA library prepared from the genome of a mycobacterium that is different from the mycobacterium used to construct the BAC-based DNA library of step a);
- 20 c) hybridizing the at least one polynucleotide of step a) to the at least one polynucleotide of step b);
- d) selecting the at least one polynucleotide of step a) that has not formed a hybrid complex with the at least one polynucleotide of step b);
- e) characterizing the selected polynucleotide.

Following the above procedure, the at least one polynucleotide of step a) may be prepared as follows :

- 30 1) digesting at least one recombinant BAC clone by an appropriate restriction endonuclease in order to isolate the polynucleotide insert of interest from the vector genetic material;
- 2) optionally amplifying the resulting polynucleotide insert;

3) optionally digesting the polynucleotide insert of step 1) or step 2) with at least one restriction endonuclease.

The above method of the invention allows the one skilled in the art to perform comparative genomics between different strains or species of mycobacteria cells, for example between pathogenic strains or species and their non pathogenic strains or species counterparts, as it is the illustrative case for the genomic comparison between *Mycobacterium tuberculosis* and *Mycobacterium bovis* BCG that is described herein in the examples.

10 Restriction digests of a given clone of a BAC library according to the invention may be blotted to membranes, and then probed with radiolabeled DNA from another strain or another species of mycobacteria, allowing the one skilled in the art to identify, characterize and isolate a polynucleotide of interest that may be involved in important metabolical and/or physiological pathways of the mycobacterium under testing, such as a polynucleotide functionally involved in 15 the pathogenicity of said given mycobacteria for its host organism.

More specifically, the inventors have shown in Example 6 that when 20 restriction digests of a given clone of the BAC library identified by the CNCM accession number I-1945 are blotted to membranes and then probed with radiolabeled total genomic DNA from, for example, *Mycobacterium bovis* BCG Pasteur, it is observed that restriction fragments that fail to hybridize with the *M. bovis* BCG Pasteur DNA are absent from its genome, hence identifying 25 polymorphic regions between *M. bovis* BCG Pasteur and *M. tuberculosis* H37Rv.

Thus, a further object of the present invention consists in a polynucleotide of interest that has been isolated according to the method described herein before.

25 In Example 6, a polynucleotide of approximately 12.7 kilobases has been isolated that is present in the genome of *M. tuberculosis* but is absent of the genome of *M. bovis* BCG. This polynucleotide of interest contains 11 ORFs that may be involved in polysaccharide biosynthesis. In particular, two of said ORFs are of particular interest, namely ORF6 (MTCY277.33; Rv1511) that encodes a 30 protein that shares significant homology with bacterial GDP-D-mannose dehydratases, whereas the protein encoded by ORF7 (MTCY277.34; Rv1512) shares significant homology with a nucleotide sugar epimerase. As polysaccharide is a major constituent of the mycobacterial cell wall, these deleted genes may cause the cell wall of *M. bovis* BCG to differ from that of *M. tuberculosis*, a fact that may have important consequences for both the immune 35

response to *M. bovis* BCG and virulence. Detection of such a polysaccharide is of diagnostic interest and possibly useful in the design of tuberculosis vaccines.

Consequently, the polynucleotide of interest obtained following the method according to the invention may contain at least one ORF, said ORF 5 preferably encoding all or part of a polypeptide involved in an important metabolical and/or physiological pathway of the mycobacteria under testing, and more specifically all or part of a polypeptide that is involved in the pathogenicity of the mycobacteria under testing, such as for example *Mycobacterium tuberculosis*, and more generally mycobacteria belonging to the *Mycobacterium tuberculosis* complex. 10

The *Mycobacterium tuberculosis* complex has its usual meaning, i.e. the complex of mycobacteria causing tuberculosis which are *Mycobacterium tuberculosis*, *Mycobacterium bovis*, *Mycobacterium africanum*, *Mycobacterium microti* and the vaccine strain *Mycobacterium bovis* BCG.

15 An illustrative polynucleotide of interest according to the present invention comprises all or part of the polynucleotide of approximately 12.7 kilobases that is present in the genome of *M. tuberculosis* but is absent from the genome of *M. bovis* BCG disclosed hereinbefore. This polynucleotide is contained in clone Rv58 of the BAC DNA library I-1945.

20 Generally, the invention also pertains to a purified polynucleotide comprising the DNA insert contained in a recombinant BAC vector belonging to a BAC-based mycobacterial genomic DNA library, such as for example the I-1945 BAC DNA library.

25 Advantageously, such a polynucleotide has been identified according to the method of the invention.

Such a polynucleotide of interest may be used as a probe or a primer useful for specifically detecting a given mycobacterium of interest, such as *Mycobacterium tuberculosis* or *Mycobacterium bovis* BCG.

30 More specifically, the invention then deals with a purified polynucleotide useful as probe or a primer comprising all or part of the nucleotide sequence SEQ ID N°1.

35 The location, on the *Mycobacterium tuberculosis* chromosome, of the above polynucleotide of sequence SEQ ID N°1 has now been ascribed to begin, at its 5'end at nucleotide at position nt 1696015 and to end, at its 3'end, at nucleotide at position nt 1708746.

For diagnostic purposes, this 12.7 kb deletion should allow a rapid PCR screening of tubercle isolates to identify whether they are bovine or human strains. The primers listed in Table 1 are flanking the deleted region and give a 722 bp amplicon in *M. bovis* or *M. bovis* BCG strains, but a fragment of 13,453 bp in *M. tuberculosis* that is practically impossible to amplify under the same PCR conditions. More importantly, assuming that some of the gene products from this region represent proteins with antigenic properties, it could be possible to develop a test that can reliably distinguish between the immune response induced by vaccination with *M. bovis* BCG vaccine strains and infection with *M. tuberculosis* or that the products (e.g. polysaccharides) are specific immunogens.

The invention also provides for a purified polynucleotide useful as a probe or as a primer, said polynucleotide being chosen in the following group of polynucleotides :

- a) a polynucleotide comprising at least 8 consecutive nucleotides of the sequence SEQ ID N°1;
- b) a polynucleotide whose sequence is fully complementary to the sequence of the polynucleotide defined in a);
- c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).

For the purpose of defining a polynucleotide or oligonucleotide hybridizing under stringent hybridization conditions, such as above, it is intended a polynucleotide that hybridizes with a reference polynucleotide under the following hybridization conditions.

The hybridization step is realized at 65°C in the presence of 6 x SSC buffer, 5 x Denhardt's solution, 0,5% SDS and 100µg/ml of salmon sperm DNA.

For technical information, 1 x SSC corresponds to 0.15 M NaCl and 0.05M sodium citrate; 1 x Denhardt's solution corresponds to 0.02% Ficoll, 0.02% polyvinylpyrrolidone and 0.02% bovine serum albumin.

The hybridization step is followed by four washing steps :

- two washings during 5 min, preferably at 65°C in a 2 x SSC and 0.1%SDS buffer,
- one washing during 30 min, preferably at 65°C in a 2 x SSC and 0.1% SDS buffer,
- one washing during 10 min, preferably at 65°C in a 0.1 x SSC and 0.1%SDS buffer.

A first illustrative useful polynucleotide that is included in the polynucleotide of sequence SEQ ID N°1 is the polynucleotide of sequence SEQ ID N°2 that corresponds to the Sp6 end-sequence of SEQ ID N°1.

5 A second illustrative useful polynucleotide that is included in the polynucleotide of sequence SEQ ID N°1 is the polynucleotide of sequence SEQ ID N°3 that corresponds to the T7 end-sequence of SEQ ID N°1, located on the opposite strand.

10 The polynucleotide of sequence SEQ ID N°1 contains 11 ORFs, the respective locations of which, taking into account the orientation of each ORF on the chromosome, on the sequence of the *Mycobacterium tuberculosis* chromosome, is given hereafter :

- The location of ORF1 is comprised between nucleotide at position nt 1695944 and nucleotide at position nt1696441.
- The location of ORF2 is comprised between nucleotide at position nt 1696728 and nucleotide at position nt1697420.
- The location of ORF3 is comprised between nucleotide at position nt 1698096 and nucleotide at position nt1699892. ORF3 probably encodes a protein having the characteristics of a membrane protein.
- The location of ORF4 is comprised between nucleotide at position nt 1700210 and nucleotide at position nt1701088.
- The location of ORF5 is comprised between nucleotide at position nt 1701293 and nucleotide at position nt1702588. ORF5 encodes a protein having the characteristics of a membrane protein.
- The location of ORF6 is comprised between nucleotide at position nt 1703072 and nucleotide at position nt1704091. ORF6 encodes a protein having the characteristics of a GDP-D-mannose dehydratase.
- The location of ORF7 is comprised between nucleotide at position nt 1704091 and nucleotide at position nt1705056. ORF7 encodes a protein having the characteristics of a nucleotide sugar epimerase involved in colanic acid biosynthesis.
- The location of ORF8 is comprised between nucleotide at position nt 1705056 and nucleotide at position nt1705784.
- The location of ORF9 is comprised between nucleotide at position nt 1705808 and nucleotide at position nt1706593. ORF9 encodes a protein having the characteristics of colanic acid biosynthesis glycosyl transferase.

- The location of ORF10 is comprised between nucleotide at position nt 1706631 and nucleotide at position nt1707524.
- The location of ORF11 is comprised between nucleotide at position nt 1707530 and nucleotide at position nt1708648. ORF11 encodes a protein similar to a spore 5 coat polysaccharide biosynthesis.

A polynucleotide of interest obtained by the above-disclosed method according to the invention may also contain at least one ORF that encodes all or part of acidic, glycine-rich proteins, belonging to the PE and PPE families, whose genes are often clustered and based on multiple copies of the polymorphic 10 repetitive sequences. The names PE and PPE derive from the fact that the motifs ProGlu (PE, positions 8, 9) and ProProGlu (PPE, positions 7 to 9) are found near the N-terminus in almost all cases. The PE protein family all have a highly conserved N-terminal domain of ~110 amino acid residues, that is predicted to have a globular structure, followed by a C-terminal segment which varies in size, 15 sequence and repeat copy number. Phylogenetic analysis separated the PE family into several groups, the larger of which is the highly repetitive PGRS class containing 55 members whereas the other groups share very limited sequence similarity in their C-terminal domains. The predicted molecular weights of the PE proteins vary considerably as a few members only contain the ~110 amino acid 20 N-terminal domain while the majority have C-terminal extensions ranging in size from 100 up to >1400 residues. A striking feature of the PGRS proteins is their exceptional glycine content (up to 50%) due to the presence of multiple tandem repetitions of GlyGlyAla or GlyGlyAsn motifs or variations thereof.

Like the PE family, the PPE protein family also has a conserved N- 25 terminal domain that comprises ~180 amino acid residues followed by C-terminal segments that vary considerably in sequence and length. These proteins fall into at least three groups, one of which constitutes the MPTR class characterised by the presence of multiple, tandem copies of the motif AsnXGlyXGlyAsnXGly. The second subgroup contains a characteristic, well-conserved motif around 30 position 350 (GlyXXSerValProXXTrp), whereas the other group contains proteins that are unrelated except for the presence of the common 180-residue PPE domain. C-terminal extensions may range in size from 00 up to 3500 residues.

One member of the PGRS sub-family, the WHO antigen 22T (Abou-Zeid 35 et al., 1991), a 55kD protein capable of binding fibronectin, is produced during

disease and elicits a variable antibody response suggesting either that individuals mount different immune responses or that this PGRS-protein may not be produced in this form by all strains of *M. tuberculosis*. In other words, at least some PE\_PGRS coding sequences encode for proteins that are involved in the 5 recognition of *M. tuberculosis* by the immune system of the infected host. Therefore, differences in the PGRS sequences could represent the principal source of antigenic variation in the otherwise genetically and antigenically homogeneous bacterium.

By performing the method of the invention using the *M. tuberculosis* BAC 10 based DNA library I-1945, the inventors have discovered the occurrence of sequence differences between a given PGRS encoding ORF (ORF reference on the genomic sequence of *M. tuberculosis* Rv0746) of *M. tuberculosis* and its counterpart sequence in the genome of *M. bovis* BCG.

More precisely, the inventors have determined that one ORF contained in 15 BAC vector N° Rv418 of the *M. tuberculosis* BCG I-1945 DNA library carries both base additions and base deletions when compared with the corresponding ORF in the genome of *M. bovis* BCG that is contained in the BAC vector N° X0175 of the *M. bovis* BCG I-XXXX DNA library. The variations observed in the base sequences correspond to variations in the C-terminal part of the aminoacid 20 sequence of the PGRS ORF translation product.

As shown in Figure 6, an amino acid stretch of 9 residues in length is present in this *M. tuberculosis* PGRS (ORF reference Rv0746) and is absent from the ORF counterpart of *M. bovis* BCG, namely the following amino acid sequence:

25 NH<sub>2</sub>-GGAGGAGGSSAGGGAGGAGGAGGWLLGD-COOH.

Furthermore, Figure 6 shows also that an amino acid stretch of 45 residues in length is absent from this *M. tuberculosis* PGRS and is present in the ORF counterpart of *M. bovis* BCG, namely following amino acid sequence:

NH<sub>2</sub>-GAGGIGGIGGNANGAGGNGGTGGQLWGSGGAGVEGGAAL  
30 SVGDT-COOH.

Similar observations were made with PPE ORF Rv0442, which showed a 5 codon deletion relative to a *M. bovis* amino acid sequence.

Given that the polymorphism associated with the PE-PGRS or PEE ORFs resulted in extensive antigenic variability or reduced antigen presentation, this 35 would be of immense significance for vaccine design, for understanding

protective immunity in tuberculosis and, possibly, explain the varied responses seen in different BCG vaccination programmes.

There are several striking parallels between the PGRS proteins and the Epstein-Barr virus-encoded nuclear antigens (EBNA). Both polypeptide families 5 are glycine-rich, contain Gly-Ala repeats that represent more than one third of the molecule, and display variation in the length of the repeat region between different isolates. The Gly-Ala repeat region of EBNA1 has been shown to function as a *cis*-acting inhibitor of antigen processing and MHC class I-restricted antigen presentation (Levitskaya et al., 1995). The fact that MHC class 10 I knock-out mice are extremely susceptible to *M. tuberculosis* underlines the importance of MHC class I antigen presentation in protection against tuberculosis. Therefore, it is possible that the PE/PPE protein family also play some role in inhibiting antigen presentation, allowing the bacillus to hide from the host's immune system.

15 As such the novel and nonobvious PGRS polynucleotide from *M. bovis* which is homolog to the *M. tuberculosis* ORF Rv0746, and which is contained in the BAC clone N° X0175 (See Table 4 for SP6 and T7 end-sequences of clone n° X0175) of the I-XXXX *M. bovis* BCG BAC DNA library is part of the present invention, as it represents a starting material in order to define specific probes or 20 primers useful for detection of antigenic variability in mycobacterial strains, possible inhibition of antigen processing as well as to differentiate *M. tuberculosis* from *M. bovis* BCG.

Thus, a further object of the invention consists in a polynucleotide comprising the sequence SEQ ID N°4.

25 Polynucleotides of interest have been defined by the inventors as useful detection tools in order to differentiate *M. tuberculosis* from *M. bovis* BCG. Such polynucleotides are contained in the 45 aminoacid length coding sequence that is present in *M. bovis* BCG but absent from *M. tuberculosis*. This polynucleotide has a sequence beginning (5'end) at the nucleotide at position nt 729 of the 30 sequence SEQ ID N°4 and ending (3'end) at the nucleotide in position nt 863 of the sequence SEQ ID N°4.

Thus, part of the present invention is also a polynucleotide which is chosen among the following group of polynucleotides :

35 a) a polynucleotide comprising at least 8 consecutive nucleotides of the nucleotide sequence SEQ ID N°5 ;

- b) a polynucleotide which sequence is fully complementary to the sequence of the polynucleotide defined in a) ;
- c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).

5 The stringent hybridization conditions for the purpose of defining the above disclosed polynucleotide are defined herein before in the specification.

10 The invention also provides for a BAC-based *Mycobacterium tuberculosis* strain H37Rv genomic DNA library that has been deposited in the Collection Nationale de Cultures de Microorganismes on November 19, 1997 under the accession number I-1945.

A further object of the invention consists in a recombinant BAC vector which is chosen among the group consisting of the recombinant BAC vectors belonging to the BAC-based DNA library I-1945.

15 Generally, a recombinant BAC vector of interest may be chosen among the following set or group of BAC vectors contained in the BAC-based DNA library I-1945 :

Rv101; Rv102; Rv103; Rv104; Rv105; Rv106; Rv107; Rv108; Rv109; Rv10;  
Rv110; Rv111; Rv112; Rv113; Rv114; Rv115; Rv116; Rv117; Rv118; Rv119;  
Rv11; Rv120; Rv121; Rv122; Rv123; Rv124; Rv126; Rv127; Rv128; Rv129;  
20 Rv130; Rv132; Rv134; Rv135; Rv136; Rv137; Rv138; Rv139; Rv13; Rv140;  
Rv141; Rv142; Rv143; Rv144; Rv145; Rv146; Rv147; Rv148; Rv149; Rv14;  
Rv150; Rv151; Rv152; Rv153; Rv154; Rv155; Rv156; Rv157; Rv159; Rv15;  
Rv160; Rv161; Rv162; Rv163; Rv164; Rv165; Rv166; Rv167; Rv169; Rv16;  
Rv170; Rv171; Rv172; Rv173; Rv174; Rv175; Rv176; Rv177; Rv178; Rv179;  
25 Rv17; Rv180; Rv181; Rv182; Rv183; Rv184; Rv185; Rv186; Rv187; Rv188;  
Rv18; Rv190; Rv191; Rv192; Rv193; Rv194; Rv195; Rv196; Rv19; Rv1; Rv201;  
Rv204; Rv205; Rv207; Rv209; Rv20; Rv214; Rv215; Rv217; Rv218; Rv219;  
Rv21; Rv220; Rv221; Rv222; Rv223; Rv224; Rv225; Rv226; Rv227; Rv228;  
Rv229; Rv22; Rv230; Rv231; Rv232; Rv233; Rv234; Rv235; Rv237; Rv240;  
30 Rv241; Rv243; Rv244; Rv245; Rv246; Rv247; Rv249; Rv24; Rv251; Rv252;  
Rv253; Rv254; Rv255; Rv257; Rv258; Rv259; Rv25; Rv260; Rv261; Rv262;  
Rv263; Rv264; Rv265; Rv266; Rv267; Rv268; Rv269; Rv26; Rv270; Rv271;  
Rv272; Rv273; Rv274; Rv275; Rv276; Rv277; Rv278; Rv279; Rv27; Rv280;  
Rv281; Rv282; Rv283; Rv284; Rv285; Rv286; Rv287; Rv288; Rv289; Rv28;  
35 Rv290; Rv291; Rv292; Rv293; Rv294; Rv295; Rv296; Rv29; Rv2; Rv301;

Rv302; Rv303; Rv304; Rv306; Rv307; Rv308; Rv309; Rv30; Rv310; Rv311; Rv312; Rv313; Rv314; Rv315; Rv316; Rv317; Rv318; Rv319; Rv31; Rv32; Rv322; Rv327; Rv328; Rv329; Rv32; Rv330; Rv331; Rv333; Rv334; Rv335; Rv336; Rv337; Rv338; Rv339; Rv33; Rv340; Rv341; Rv343; Rv344; Rv346; 5 Rv347; Rv348; Rv349; Rv34; Rv350; Rv351; Rv352; Rv353; Rv354; Rv355; Rv356; Rv357; Rv358; Rv359; Rv35; Rv360; Rv361; Rv363; Rv364; Rv365; Rv366; Rv367; Rv368; Rv369; Rv36; Rv370; Rv371; Rv373; Rv374; Rv375; Rv376; Rv377; Rv378; Rv379; Rv37; Rv381; Rv382; Rv383; Rv384; Rv385; Rv386; Rv387; Rv388; Rv389; Rv38; Rv390; Rv391; Rv392; Rv393; Rv396; 10 Rv39; Rv3; Rv40; Rv412; Rv413; Rv414; Rv415; Rv416; Rv417; Rv418; Rv419; Rv41; Rv42; Rv43; Rv44; Rv45; Rv46; Rv47; Rv48; Rv49; Rv4; Rv50; Rv51; Rv52; Rv53; Rv54; Rv55; Rv56; Rv57; Rv58; Rv59; Rv5; Rv60; Rv61; Rv62; Rv63; Rv64; Rv65; Rv66; Rv67; Rv68; Rv69; Rv6; Rv70; Rv71; Rv72; Rv73; Rv74; Rv75; Rv76; Rv77; Rv78; Rv79; Rv7; Rv80; Rv81; Rv82; Rv83; Rv84; 15 Rv85; Rv86; Rv87; Rv88; Rv89; Rv8; Rv90; Rv91; Rv92; Rv94; Rv95; Rv96; Rv9.

The end sequences of the polynucleotide inserts of each of the above clones corresponding respectively to the sequences adjacent to the T7 promoter and to the Sp6 promoter on the BAC vector are shown in Table 3.

20 It has been shown by the inventors that the minimal overlapping set of BAC vectors of the BAC-based DNA library I-1945 contains 68 unique BAC clones and practically spans almost the whole H37Rv chromosome with the exception of a single gap of approximately 150 kb.

More specifically, a recombinant BAC vector of interest is chosen among 25 the following set or group of BAC vectors from the BAC-based DNA library I-1945, the location of which vector DNA inserts on the chromosome of *M. tuberculosis* is shown in Figure 3 :

Rv234; Rv351; Rv166; Rv35; Rv415; Rv404; Rv209; Rv272; Rv30; Rv228; Rv233; Rb38; Rv280; Rv177; Rv48; Rv374; Rv151; Rv238; Rv156; Rv92; Rv3; 30 Rv403; Rv322; Rv243; Rv330; Rv285; Rv233; Rv219; Rv416; Rv67; Rv222; Rv149; Rv279; Rv87; Rv273; Rv266; Rv25; Rv136; Rv414; Rv13; Rv289; Rv60; Rv104; Rv5; Rv165; Rv215; Rv329; Rv240; Rv19; Rv74; Rv411; Rv167; Rv56; Rv80; Rv164; Rv59; Rv313; Rv265; Rv308; Rv220; Rv258; Rv339; Rv121; Rv419; Rv418; Rv45; Rv217; Rv134; Rv17; Rv103; Rv21; Rv22; Rv2; Rv270; 35 Rv267; Rv174; Rv257; Rv44; Rv71; Rv7; Rv27; Rv191; Rv230; Rv128; Rv407;

Rv106; Rv39; Rv255; Rv74; Rv355; Rv268; Rv58; Rv173; Rv264; Rv417; Rv401; Rv144; Rv302; Rv81; Rv163; Rv281; Rv221; Rv420; Rv175; Rv86; Rv412; Rv73; Rv269; Rv214; Rv287; Rv42; Rv143.

5 The polynucleotides disclosed in Table 3 may be used as probes in order to select a given clone of the BAC DNA library I-1945 for further use.

The invention also provides for a BAC-based *Mycobacterium bovis* strain Pasteur genomic DNA library that has been deposited in the Collection Nationale de Cultures de Microorganismes on XXXX XX, 1998 under the accession number I-XXXX.

10 A further object of the invention consists in a recombinant BAC vector which is chosen among the group consisting of the recombinant BAC vectors belonging to the BAC-based DNA library I-XXXX. This DNA library contains approximately 1600 clones. The average insert size is estimated to be ~80 kb.

15 Generally, a recombinant BAC vector of interest may be chosen among the following set or group of BAC vectors contained in the BAC-based DNA library I-XXXX :

X0001; X0002; X0003; X0004; X0006; X0007; X0008; X0009; X0010; X0012; X0013; X0014; X0015; X0016; X0017; X0018; X0019; X0020; X0021; X0175.

20 The end sequences of the polynucleotide inserts of each of the above clones corresponding respectively to the sequences adjacent to the T7 promoter and to the Sp6 promoter on the BAC vector are shown in Table 4.

The polynucleotides disclosed in Table 4 may be used as probes in order to select a given clone of the BAC DNA library I-XXXX for further use.

25 Are also part of the invention the polynucleotide inserts that are contained in the above described BAC vectors, that are useful as primers or probes.

These polynucleotides and nucleic acid fragments may be used as primers for use in amplification reactions, or as nucleic probes.

30 PCR is described in the US patent N° 4,683,202. The amplified fragments may be identified by an agarose or a polyacrylamide gel electrophoresis, or by a capillary electrophoresis or alternatively by a chromatography technique (gel filtration, hydrophobic chromatography or ion exchange chromatography). The specificity of the amplification may be ensured by a molecular hybridization using, for example, one of the initial primers as nucleic probes.

35 Amplified nucleotide fragments are used as probes in hybridization reactions in order to detect the presence of one polynucleotide according to the

present invention or in order to detect mutations in the genome of the given mycobacterium of interest, specifically a mycobacterium belonging to the *Mycobacterium tuberculosis* complex and more specifically *Mycobacterium tuberculosis* and *Mycobacterium bovis* BCG.

5 Are also part of the present invention the amplified nucleic fragments (« amplicons ») defined herein above.

These probes and amplicons may be radioactively or non-radioactively labeled, using for example enzymes or fluorescent compounds.

10 Other techniques related to nucleic acid amplification may also be used and are generally preferred to the PCR technique.

15 The Strand Displacement Amplification (SDA) technique (Walker et al., 1992) is an isothermal amplification technique based on the ability of a restriction enzyme to cleave one of the strands at his recognition site (which is under a hemiphosphorothioate form) and on the property of a DNA polymerase to initiate the synthesis of a new strand from the 3'OH end generated by the restriction enzyme and on the property of this DNA polymerase to displace the previously synthesized strand being localized downstream. The SDA method comprises two main steps :

20 a) The synthesis, in the presence of dCTP-alpha-S, of DNA molecules that are flanked by the restriction sites that may be cleaved by an appropriate enzyme.

25 b) The exponential amplification of these DNA molecules modified as such, by enzyme cleavage, strand displacement and copying of the displaced strands. The steps of cleavage, strand displacement and copy are repeated a sufficient number of times in order to obtain an accurate sensitivity of the assay.

30 The SDA technique was initially realized using the restriction endonuclease HincII but is now generally practised with an endonuclease from *Bacillus stearothermophilus* (BSOBI) and a fragment of a DNA polymerase which is devoid of any 5'→3' exonuclease activity isolated from *Bacillus cladotetanax* (exo- Bca) [=exo-minus-Bca]. Both enzymes are able to operate at 60°C and the system is now optimized in order to allow the use of dUTP and the decontamination by UDG. When using this technique, as described by Spargo et al. in 1996, the doubling time of the target DNA is of 26 seconds and the amplification rate is of 10<sup>10</sup> after an incubation time of 15 min at 60°C.

The SDA amplification technique is more easy to perform than PCR (a single thermostated waterbath device is necessary) and is faster than the other amplification methods.

Thus, another object of the present invention consists in using the nucleic acid fragments according to the invention (primers) in a method of DNA or RNA amplification according to the SDA technique. For performing SDA, two pairs of primers are used : a pair of external primers (B1, B2) consisting of a sequence specific for the target polynucleotide of interest and a pair of internal primers (S1, S2) consisting of a fusion oligonucleotide carrying a site that is recognized by a restriction endonuclease, for example the enzyme BSOBI.

The operating conditions to perform SDA with such primers are described in Spargo et al, 1996.

The polynucleotides of the invention and their above described fragments, especially the primers according to the invention, are useful as technical means for performing different target nucleic acid amplification methods such as :

- TAS (Transcription-based Amplification System), described by Kwok et al. in 1989.
- SR (Self-Sustained Sequence Replication), described by Guatelli et al. in 1990.
- NASBA (Nucleic acid Sequence Based Amplification), described by Kievitis et al. in 1991.
- TMA (Transcription Mediated Amplification).

The polynucleotides according to the invention are also useful as technical means for performing methods for amplification or modification of a nucleic acid used as a probe, such as :

- LCR (Ligase Chain Reaction), described by Landegren et al. in 1988 and improved by Barany et al. in 1991 who employ a thermostable ligase.
- RCR (Repair Chain Reaction) described by Segev et al. in 1992.
- CPR (Cycling Probe Reaction), described by Duck et al. in 1990.
- Q-beta replicase reaction, described by Miele et al. in 1983 and improved by Chu et al. in 1986, Lizardi et al. in 1988 and by Burg et al. and Stone et al. in 1996.

When the target polynucleotide to be detected is a RNA, for example a mRNA, a reverse transcriptase enzyme will be used before the amplification reaction in order to obtain a cDNA from the RNA contained in the biological sample. The generated cDNA is subsequently used as the nucleic acid target for

the primers or the probes used in an amplification process or a detection process according to the present invention.

5 The non-labeled polynucleotides or oligonucleotides of the invention may be directly used as probes. Nevertheless, the polynucleotides or oligonucleotides are generally labeled with a radioactive element ( $^{32}\text{P}$ ,  $^{35}\text{S}$ ,  $^3\text{H}$ ,  $^{125}\text{I}$ ) or by a non-isotopic molecule (for example, biotin, acetylaminofluorene, digoxigenin, 5-bromodesoxyuridin, fluorescein) in order to generate probes that are useful for numerous applications.

10 Examples of non-radioactive labeling of nucleic acid fragments are described in the french patent N° FR-7810975 or by Urdea et al. or Sanchez-Pescador et al., 1988.

15 In the latter case, other labeling techniques may be also used such as those described in the french patents FR-2 422 956 and 2 518 755. The hybridization step may be performed in different ways (Matthews et al., 1988). The more general method consists of immobilizing the nucleic acid that has been extracted 20 from the biological sample onto a substrate (nitrocellulose, nylon, polystyrene) and then to incubate, in defined conditions, the target nucleic acid with the probe. Subsequently to the hybridization step, the excess amount of the specific probe is discarded and the hybrid molecules formed are detected by an appropriate method (radioactivity, fluorescence or enzyme activity measurement).

25 Advantageously, the probes according to the present invention may have structural characteristics such that they allow the signal amplification, such structural characteristics being, for example, branched DNA probes as those described by Urdea et al. in 1991 or in the European patent N° EP-0 225 807 (Chiron).

30 In another advantageous embodiment of the probes according to the present invention, the latters may be used as « capture probes », and are for this purpose immobilized on a substrate in order to capture the target nucleic acid contained in a biological sample. The captured target nucleic acid is subsequently detected with a second probe which recognizes a sequence of the target nucleic acid which is different from the sequence recognized by the capture probe.

35 The oligonucleotide probes according to the present invention may also be used in a detection device comprising a matrix library of probes immobilized on a substrate, the sequence of each probe of a given length being localized in a shift of one or several bases, one from the other, each probe of the matrix library thus

being complementary to a distinct sequence of the target nucleic acid. Optionally, the substrate of the matrix may be a material able to act as an electron donor, the detection of the matrix positons in which an hybridization has occurred being subsequently determined by an electronic device. Such matrix libraries of probes and methods of specific detection of a targer nucleic acid is described in the European patent application N° EP-0 713 016 (Affymax technologies) and also in the US patent N° US-5,202,231 (Drmanac).

Since almost the whole length of a mycobacterial chromososome is covered by a BAC-based genomic DNA libraries according to the present invention (i.e. 97% of the *M. tuberculosis* chromosome is covered by the BAC library I-1945), these DNA libraries will play an important role in a plurality of post-genomic applications, such as in mycobacterial gene expression studies where the canonical set of BACs could be used as a matrix for hybridization studies. Probing such matrices with cDNA probes prepared from total mRNA will uncover genetic loci induced or repressed under different physiological conditions (Chuang et al., 1993; Trieselmann et al., 1992). As such, the H37Rv BAC library represents a fundamental resource for present and future genomics investigations.

The BAC vectors or the polynucleotide inserts contained therein may be directly used as probes, for example when immobilized on a substrate such as described herein before.

The BAC vectors or their polynucleotide inserts may be directly adsorbed on a nitrocellulose membrane, at predetermined locations on which one or several polynucleotides to be tested are then put to hybridize therewith.

Preferably, a collection of BAC vectors that spans the whole genome of the mycobacterium under testing will be immobilized, such as, for example, the set of 68 BAC vectors of the I-1945 DNA library that is described elsewhere in the specification and shown in Figure 3.

The immobilization and hybridization steps may be performed as described in the present Materials and Methods Section.

As another illustrative embodiment of the use of the BAC vectors of the invention as polynucleotide probes, these vectors may be useful to perform a transcriptional activity analysis of mycobacteria growing in different environmental conditions, for example under conditions in which a stress response is expected, as it is the case at an elevated temperature, for example 40°C.

In this specific embodiment of the invention, Genescreen membranes may be used to immobilize the restriction endonuclease digests (*Hind*III digests for the BAC DNA library I-1945) of the BAC vectors by transfer from a gel (Trieselmann et al., 1992).

5        Alternatively, the BAC vectors may be immobilized for dot blot experiments as follows. First, the DNA concentration of each BAC clone is determined by hybridization of blots of clone DNAs and of a BAC vector concentration standard with a BAC vector specific DNA probe. Hybridization is quantified by the Betascope 603 blot analyzer (Betagen Corp.), which collects 10 beta particles directly from the blot with high efficiency. Then, 0.5 µg of each clone DNA is incubated in 0.25 M NaOH and 10 mM EDTA at 65°C for 60 min to denature the DNA and degrade residual RNA contaminants. By using a manifold filtration system (21 by 21 wells), each clone DNA is blotted onto a GeneScreen Plus nylon membrane in the alkaline solution. After neutralization, 15 the blots are baked at 85°C for 2 h under vacuum. Positive and negative controls are added when necessary. In order to perform this procedure, it may be referred to the article of Chuang et al. (1993).

For RNA extractions, cells grown in a suitable volume of culture medium may, for example, be immediately mixed with an equal volume of crushed ice at - 20 70°C and spun at 4°C in a 50 ml centrifugation tube. The cell pellet is then suspended in 0.6 ml of ice-cold buffer (10 mM KCl, 5 mM MgCl<sub>2</sub>, 10 mM Tris; pH 7.4) and then immediately added to 0.6 ml of hot lysis buffer (0.4 M NaCl, 40 mM EDTA, 1% beta-mercaptoethanol, 1% SDS, 20 mM Tris; pH 7.4) containing 100 µl of water saturated phenol. This mixture is incubated in a boiling water 25 bath for 40 s. The debris are removed by centrifugation. The supernatant is extracted with phenol-chloroform five times, ethanol precipitated, and dried. The dried RNA pellet is dissolved in water before use.

Then labeled total cDNA may be prepared by the following method. The reaction mixture contains 15 µg of the previously prepared total RNA, 5 µg of 30 pd(N<sub>6</sub>) (random hexamers from Pharmacia Inc.), 0.5 mM dATP, 0.5 mM dGTP and 0.5mM DTTP, 5µM dCTP, 100 µCi of [ $\alpha$ -<sup>32</sup>P]dCTP (3,000 Ci/mmol), 50 mM Tris-HCl (pH 8.3), 6 mM MgCl<sub>2</sub>, 40 mM KCl, 0.5 U of avian myeloblastosis virus reverse transcriptase (Life Science Inc.) in a total volume of 50 µl. The reaction is allowed to continue overnight at room temperature. EDTA and NaOH 35 are then added to final concentrations of 50 mM and 0.25 M, respectively, and

the mixture is incubated at 65°C for 30 min to degrade the RNA templates. The cDNA is then ready to use after neutralization by adding HCl and Tris buffer.

The hybridization step may be performed as described by Chuang et al. (1993) and briefly disclosed hereinafter. The DNA dot blot is hybridized to <sup>32</sup>P-labeled total cDNA in a solution containing 0.1% polyvinylpyrrolidone, 0.1% Ficoll, 0.1% sodium Pp<sub>i</sub>, 0.1% bovine serum albumin, 0.5% SDS, 100 mM NaCl, and 0.1 mM sodium citrate, pH 7.2, at 65°C for 2 days and then washed with a solution containing 0.1% SDS, 100 mM NaCl, and 10 mM Na-citrate, pH 7.2. The same dot blot is used for hybridization with both control and experimental cDNAs, with an alkaline probe stripping procedure (soaked twice in 0.25M NaOH-0.75 M NaCl at room temperature, 30 min each, neutralized, and completely dried at 65°C for at least 30 min) between the two hybridizations. Quantification may be done with the Betascope 603 blot analyzer (Betagen Corp.).

As it flows from the above technical teachings, another object of the invention consists in a method for detecting the presence of mycobacteria in a biological sample comprising the steps of :

- a) bringing into contact the recombinant BAC vector or a purified polynucleotide according to the invention with a biological sample ;
- 20 b) detecting the hybrid nucleic acid molecule formed between said purified polynucleotide and the nucleic acid molecules contained within the biological sample.

The invention further deals with a method for detecting the presence of mycobacteria in a biological sample comprising the steps of :

- 25 a) bringing into contact the recombinant BAC vector or a purified polynucleotide according to the invention that has been immobilized onto a substrate with a biological sample ;
- b) bringing into contact the hybrid nucleic acid molecule formed between said purified polynucleotide and the nucleic acid contained in the biological sample
- 30 with a labeled recombinant BAC vector or a polynucleotide according to the invention, provided that said polynucleotide and polynucleotide of step a) have non-overlapping sequences.

Another object of the invention consists in a method for detecting the presence of mycobacteria in a biological sample comprising the steps of :

- a) bringing into contact the nucleic acid molecules contained in the biological sample with a pair of primers according to the invention;
- b) amplifying said nucleic acid molecules;
- c) detecting the nucleic acid fragments that have been amplified, for example by gel electrophoresis or with a labeled polynucleotide according to the invention.

5 In one specific embodiment of the above detection and/or amplification methods, said methods comprise an additional step wherein before step a), the nucleic acid molecules of the biological sample have been made available to a hybridization reaction.

10 In another specific embodiment of the above detection methods, said methods comprise an additional step, wherein, before the detection step, the nucleic acid molecules that are not hybridized with the immobilized purified polynucleotide are removed.

15 Also part of the invention is a kit for detecting mycobacteria in a biological sample comprising :

- a) a recombinant BAC vector or a purified polynucleotide according to the invention;
- b) reagents necessary to perform a nucleic acid hybridization reaction.

20 The invention also pertains to a kit for detecting a mycobacteria in a biological sample comprising :

- a) a recombinant BAC vector or a purified polynucleotide according to the invention that is immobilized onto a substrate;
- b) reagents necessary to perform a nucleic acid hybridization reaction;
- c) a purified polynucleotide according to the invention which is radioactively or 25 non-radioactively labeled, provided that said polynucleotide and the polynucleotide of step a) have non-overlapping sequences.

Moreover, the invention provides for a kit for detecting mycobacteria in a biological sample comprising :

- a) a pair of purified primers according to the invention;
- b) reagents necessary to perform a nucleic acid amplification reaction;
- c) optionally, a purified polynucleotide according to the invention useful as a probe.

30 The invention embraces also a method for detecting the presence of a genomic DNA, a cDNA or a mRNA of mycobacteria in a biological sample. 35 comprising the steps of :

- a) bringing into contact the biological sample with a plurality of BAC vectors according to the invention or purified polynucleotides according to the invention, that are immobilized on a substrate;
- b) detecting the hybrid complexes formed.

5 The invention also provides a kit for detecting the presence of genomic DNA, cDNA or mRNA of a mycobacterium in a biological sample, comprising :  
a) a substrate on which a plurality of BAC vectors according to the invention or purified polynucleotides according to the invention have been immobilized;  
b) optionally, the reagents necessary to perform the hybridization reaction.

10 Additionally, the recombinant BAC vectors according to the invention and the polynucleotide inserts contained therein may be used for performing detection methods based on « molecular combing ». Said methods consist in methods for aligning macromolecules, especially DNA and are applied to processes for detecting, for measuring intramolecular distance, for separating and/or for 15 assaying a macromolecule, especially DNA in a sample.

20 These « molecular combing » methods are simple methods, where the triple line S/A/B (meniscus) resulting from the contact between a solvent A and the surface S and a medium B is caused to move on the said surface S, the said macromolecules (i.e. DNA) having a part, especially an end, anchored on the 25 surface S, the other part, especially the other end, being in solution in the solvent A. These methods are particularly fully described in the PCT Application n° PCT/FR 95/00165 filed on February 11, 1994 (Bensimon et al.).

When performing the « molecular combing » method with the recombinant BAC vectors according to the inventions or their polynucleotide inserts, the 25 latters may be immobilized (« anchored ») on a suitable substrate and aligned as described in the PCT Application n° PCT/FR 95/00165, the whole teachings of this PCT Application being herein incorporated by reference. Then, 30 polynucleotides to be tested, preferably under the form of radioactively or non radioactively labeled polynucleotides, that may consist of fragments of genomic DNA, cDNA etc. are brought into contact with the previously aligned polynucleotides according to the present invention and then their hybridization position on the aligned DNA molecules is determined using any suitable means including a microscope or a suitable camera device.

35 Thus, the present invention is also directed to a method for the detection of the presence of a polynucleotide of mycobacterial origin in a biological sample

and/or for physical mapping of a polynucleotide on a genomic DNA, said method comprising :

- a) aligning at least one polynucleotide contained in a recombinant BAC vector according to the invention on the surface of a substrate;
- 5 b) bringing into contact at least one polynucleotide to be tested with the substrate on which the at least one polynucleotide of step a) has been aligned;
- c) detecting the presence and/or the location of the tested polynucleotide on the at least one aligned polynucleotide of step a).

The invention finally provides for a kit for performing the above method, 10 comprising :

- a) a substrate whose surface has at least one polynucleotide contained in a recombinant BAC vector according to the invention;
- b) optionally, reagents necessary for labeling DNA;
- c) optionnally, reagents necessary for performing a hybridization reaction.

15 In conclusion, it may be underlined that the alliance of such BAC-based approaches such as described in the present specification to the advances in comparative genomics by the availability of an increased number of complete genomes, and the rapid increase of well-characterized gene products in the public databases, will allow the one skilled in the art an exhaustive analysis of the 20 mycobacterial genome.

## MATERIALS AND METHODS

1. **DNA-preparation.** Preparation of *M. tuberculosis* H37Rv DNA in agarose 25 plugs was conducted as previously described (Canard et al., 1989; Philipp et al., 1996b). Plugs were stored in 0.2 M EDTA at 4°C and washed 3 times in 0.1% Triton X-100 buffer prior to use.
2. **BAC vector preparation.** pBeloBAC11 was kindly provided by Dr. Shizuya, Department of Biology, California Institute of Technology (Pasadena, CA). The preparation followed the description of Woo et al., 1994 (Woo et al., 1994).
- 30 3. **Partial digestion with *Hind*III.** Partial digestion was carried out on plugs, each containing approximately 10 µg of high molecular weight DNA, after three one hour equilibration steps in 50 ml of *Hind*III 1X digestion buffer (Boehringer Mannheim, Mannheim, Germany) plus 0.1% Triton X-100. The buffer was then removed and replaced by 1ml/plug of ice-cold *Hind*III enzyme buffer containing 35 20 units of *Hind*III (Boehringer). After two hours incubation on ice, the plugs

were transferred to a 37°C water bath for 30 minutes. Digestions were stopped by adding 500 µl of 50 mM EDTA (pH 8.0).

4. **Size selection.** The partially digested DNA was subjected to contour-clamped homogenous electric field (CHEF) electrophoresis on a 1% agarose gel using a BioRad DR III apparatus (BioRad, Hercules, CA) in 1X TAE buffer at 13°C, with a ramp from 3 to 15 seconds at 6 V/cm for 16 hours. Agarose slices from 25 to 75 kb, 75 to 120 kb and 120 to 180 kb were excised from the gel and stored in TE at 4°C.

5. **Ligation and transformation.** Agarose-slices containing fractions from 25 to 75 kb, 75 to 120 kb and 120 to 180 kb were melted at 65°C for 10 minutes and digested with Gelase (Epicentre Technologies, Madison, WI), using 1 unit per 100 µl gel-slice. 25-100 ng of the size-selected DNA was then ligated to 10 ng of *Hind*III digested, dephosphorylated pBeloBAC11 in a 1:10 molar ratio using 10 units of T4 DNA ligase (New England Biolabs, Beverly, MA) at 16°C for 20 hours. Ligation mixtures were heated at 65°C for 15 minutes, then drop-dialysed against TE using Millipore VS 0.025 mM membranes (Millipore, Bedford, MA). 10. Fresh electrocompetent *E. coli* DH10B cells (Sheng et al., 1995) were harvested from 200 ml of a mid-log (OD<sub>550</sub>=0.5) culture grown in SOB medium. Cells 15. were washed three times in ice-cold water, and finally resuspended in ice-cold water to a cell density of 10<sup>11</sup> cells/ml (OD<sub>550</sub>=150). 1 µl of the ligation-mix 20. was used for electroporation of 30 µl of electrocompetent DH10B *E. coli* using a Eurogentec Easyject Plus electroporator (Eurogentec, Seraing, Belgium), with 25. settings of 2.5 kV, 25 µF, and 99 Ω, in 2 mm wide electroporation cuvettes. After 30. electroporation, cells were resuspended in 600 µl of SOC medium, allowed to recover for 45 minutes at 37°C with gentle shaking, and then plated on LB agar containing 12.5 µg/ml chloramphenicol (CM), 50 µg/ml X-gal, and 25 µg/ml IPTG. The plates were incubated overnight and recombinants (white colonies) 35. were picked manually to 96 well plates. Each clone was inoculated 3 times (2 X 200 µl and 1 X 100 µl of 2YT/12.5 µg/ml CM per clone) and incubated overnight. One of the microtiter plates, containing 100 µl culture per well, was maintained as a master plate at -80°C after 100 µl of 80% glycerol were added to each well, while minipreps (Sambrook et al., 1989) were prepared from the remaining two plates to check for the presence of inserts. Clones containing inserts were then designated "Rv" clones, repicked from the master plate to a second set of plates for storage of the library at -80°C.

6. **Preparation of DNA for sizing, direct sequencing and comparative genomics.** A modified Birnboim and Doly protocol (Birnboim et al., 1979) was used for extraction of plasmid DNA for sequencing purposes. Each Rv clone was inoculated into a 50 ml Falcon polypropylene tube containing 40 ml of 2YT medium with 12.5 µg/ml of CM and grown overnight at 37°C with shaking. Cells were harvested by centrifugation and stored at -20°C. The frozen pellet was resuspended in 4 ml of Solution A (50 mM glucose, 10 mM EDTA, 25 mM Tris, pH 8.0) and 4 ml of freshly prepared solution B (0.2 M NaOH, 0.2% SDS) was then added. The solution was gently mixed and kept at room temperature for 5 minutes before adding 4 ml of ice-cold solution C (3M Sodium Acetate, pH 4.7). Tubes were kept on ice for 15 min, and centrifuged at 10,000 rpm for 15 min. After isopropanol precipitation, the DNA pellet was dissolved in 600 µl RNase solution (15 mM Tris HCl pH 8.0, 10 µg/ml RNase A). After 30 minutes at 37°C the DNA solution was extracted with chloroform:isoamylalcohol (24:1) and precipitated from the aqueous phase using isopropanol. The DNA pellet was then rinsed with 70% ethanol, air-dried and dissolved in 30 µl distilled water. In general, DNA prepared by this method was clean and concentrated enough to give good quality results by automatic sequencing (at least 300 bp of sequence). For a few DNA preparations, an additional polyethylene glycol (PEG) precipitation step was necessary, which was performed as follows. The 30 µl of DNA solution were diluted to 64 µl, mixed gently and precipitated using 16 µl 4M NaCl and 80 µl of 13% PEG 8000. After 30 min on ice the tubes were centrifuged at 4°C, the pellet carefully rinsed with 70% ethanol, air-dried and diluted in 20 µl of distilled water.

7. **Sizing of inserts.** Insert sizes were determined by pulsed-field gel electrophoresis (PFGE) after cleavage with *Dra*I (Promega). 100-200 ng of DNA was *Dra*I-cleaved in 20 µl total reaction volume, following the manufacturer's recommendations, then loaded onto a 1% agarose gel and migrated using a pulse of 4 s for 15 h at 6.25 V/cm at 10°C on an LKB-Pharmacia CHEF apparatus. Mid-range and low-range PFGE markers (New England Biolabs) were used as size standards. Insert sizes were estimated after ethidium bromide staining of gels.

8. **Direct sequencing.** For each sequencing reaction 7 µl BAC DNA (300-500ng), 2 µl primer (2 µM), 8 µl reaction mix of the *Taq* DyeDeoxy Terminator cycle sequencing kit (Applied Biosystems) and 3 µl distilled water were used.

After 26 cycles (96°C for 30 sec; 56°C for 15 sec; 60°C for 4 min) in a thermocycler (MJ-research Inc., Watertown, MA) DNA was precipitated using 70 µl of 70% ethanol/0.5 mM MgCl<sub>2</sub>, centrifuged, rinsed with 70% ethanol, dried and dissolved in 2 µl of formamide/EDTA buffer. SP6 and T7 samples of 5 32 BAC clones were loaded onto 64 lane, 6% polyacrylamide gels and electrophoresis was performed on a Model 373A automatic DNA sequencer (Applied Biosystems) for 12 to 16 hours. The sequences of oligonucleotides used as primers are shown in Table 1.

9. **DOP-PCR.** As an alternate procedure we used partially degenerate 10 oligonucleotides in combination with vector-specific (SP6 or T7) primers to amplify insert ends of BAC clones, following a previously published protocol for P1 clones (Liu et al., 1995). The degenerate primers Deg2, Deg3, Deg4, Deg6 (Table 1) gave the best results for selected amplification of insert termini.

15 **Table 1:** Primers used for PCRs and sequencing

Vector specific Primers for DOP PCR- first amplification step:

SP6-BAC1: AGT TAG CTC ACT CAT TAG GCA

T7-BAC1 : GGA TGT GCT GCA AGG CGA TTA

Vector specific Primers (direct sequencing, nested primer for second PCR step)

20 SP6 Mid: AAA CAG CTA TGA CCA TGA TTA CGC CAA

T7-Belo2: TCC TCT AGA GTC GAC CTG CAG GCA

Degenerate Primers:

Deg2: TCT AGA NNN NNN TCC GGC

Deg3: TCT AGA NNN NNN GGG CCC

25 Deg4: CGT TTA AAN NNN NWA GGC CG

Deg6: GGT ACT AGT NNN NNW TCC GGC

Primers used for the amplification of *M. bovis* DNA in polymorphic chromosomal region of Rv58:

Primer 1: ACG ACC TCA TAT TCC GAA TCC C

30 Primer 2: GCA TCT GTT GAG TAC GCA CTT CC

10. **Screening by pooled PCR.** To identify particular clones in the library which could not be detected by random end-sequencing of the 400 BAC clones, PCR-screening of DNA pools was performed. Primers were designed for regions of the 35 chromosome where no BAC coverage was apparent using cosmid-or H37Rv

whole genome shotgun sequences. Primers were designed to amplify approximately 400-500 bp. Ninety-six-well plates containing 200  $\mu$ l 2YT/12.5  $\mu$ g/ml CM per well were inoculated with 5  $\mu$ l of -80°C glycerol stock cultures each from the master plates and incubated overnight. The 96 clones of 5 each plate were pooled by taking 20  $\mu$ l of culture from each well and this procedure was repeated for 31 plates. Pooled cultures were centrifuged, the pellets were resuspended in sterile water, boiled for 5 minutes, centrifuged and the supernatants kept for PCRs. As an initial screening step, the 31 pools of a total of 2976 BACs, representing about two thirds of the library were tested for 10 the presence of a specific clone using appropriate PCR primers. PCR was performed using 10  $\mu$ l of supernatant, 5  $\mu$ l of assay buffer (100 mM b-mercaptoethanol, 600 mM Tris HCl (pH 8.8), 20 mM MgCl<sub>2</sub>, 170 mM (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>), 5  $\mu$ l of Dimethylsulfoxide (DMSO), 5  $\mu$ l of dNTPs (20 mM), 5  $\mu$ l of water, 10  $\mu$ l primer (2  $\mu$ M), 10  $\mu$ l inverse primer (2  $\mu$ M) and 0.2 units of *Taq* 15 DNA polymerase (Boehringer). 32 cycles of PCR (95°C for 30 s, 55°C for 1 min 30 s, 72°C for 2 min) were performed after an initial denaturation at 95°C for 1 min. An extension step at 72 °C for 5 min finished the PCR. If a pool of 96 clones yielded an appropriate PCR product (Fig. 1A), subpools were made to identify the specific clone. Subpools representative for lane A of a 96 well plate 20 were made by pooling clones 1 to 12 from lane A into a separate tube. Subpools for lanes B to H were made in the same way. In addition, subpools of each of the 12 rows (containing 8 clones each) were made, so that for one 96 well plate, 20 subpools were obtained. PCR with these 20 subpools identified the specific clone 25 (Fig. 1B, lower gel portion). If more than one specific clone was present among the 96 clones of one plate (Fig. 1B, upper gel portion), additional PCR reactions had to be performed with the possible candidates (data not shown).

11. **Genomic comparisons.** DNA from the BAC clone Rv58 was digested with the restriction endonucleases *Eco*RI and *Pvu*II, and resolved by agarose gel electrophoresis at low voltage overnight (1.5 V/cm). DNA was transferred via the 30 method of Southern to nitrocellulose membranes (Hybond C extra, Amersham) following standard protocols (Sambrook et al., 1989), then fixed to the membranes at 80°C for 2 hours. The blot was hybridized with <sup>32</sup>P labelled total genomic DNA from *M. tuberculosis* H37Rv, *M. bovis* type strain (ATCC 19210) or *M. bovis* BCG Pasteur. Hybridization was performed at 37°C overnight in

50% formamide hybridization buffer as previously described (Philipp et al., 1996b). Results were interpreted from the autoradiograms.

12. **Computer analysis.** Sequence data from the automated sequencer ABI373A were transferred as binary data to a Digital Alpha 200 station or Sun SparcII 5 station and analysed using TED, a sequence analysis program from the Staden software package (Dear et al., 1991). Proof-read sequences were compared using the BLAST programs (Altschul et al., 1990) to the *M. tuberculosis* H37Rv sequence databases of the Sanger Centre, containing the collected cosmid sequences (TB.dbs) and whole-genome shotgun reads (TB\_shotgun\_all.dbs) 10 (<http://www.sanger.ac.uk/>). In addition, local databases containing 1520 cosmid end-sequences and the accumulating BAC end-sequences were used to determine the exact location of end-sequenced BACs on the physical and genetic map. MycDB (Bergh et al., 1994) and public databases (EMBL, Genbank) were also used to compare new sequences, but to a lesser extent. The organization of the 15 open reading frames (ORFs) in the polymorphic region of clone Rv58 was determined using the DIANA software established at the Sanger Centre.

## EXAMPLES

20 **Example 1 : Construction of a pBeloBAC11 library of *M. tuberculosis* H37Rv.**

Partial *Hind*III fragments of H37Rv DNA in the size range of 25 to 180 kb were ligated into pBeloBAC11 and electroporated into strain *E. coli* DH10B. While cloning of fractions I (25 to 75 kb) and II (75 to 120 kb) gave approximately  $4 \times 10^4$  transformants (white colonies), cloning of fraction III (120 25 to 180 kb) repeatedly resulted in empty clones. Parallel cloning experiments using partial *Hind*III digests of human DNA resulted in stable inserts for all three fractions (data not shown), suggesting that the maximum size of large inserts in BAC clones is strongly dependent on the source of the DNA. Analysis of the 30 clones for the presence of inserts revealed that 70 % of the clones had an insert of the appropriate size while the remaining 30% of white colonies represented empty or *lacZ*'-mutated clones. Size determination of randomly selected, *Dra*I-cleaved BACs via PFGE showed that the insert sizes ranged for the majority of the clones between 40 kb and 100 kb with an average size of 70 kb. Clones with 35 inserts of appropriate size were designated with "Rv" numbers, recultured and stored at -80°C for further use.

**Example 2 : Direct DNA sequence analysis of BACs.**

To characterize the BAC clones, they were systematically subjected to insert termini sequencing. Two approaches, direct sequencing of BAC DNA and PCR with degenerate oligonucleotide primers (DOP), adapted to the high G+C content of mycobacterial DNA, were used. In a first screening phase, 50 BAC clones designated Rv1 to Rv50 were analysed using both methods in parallel. Except for two clones, where the sequences diverged significantly, the sequences obtained by the two methods only differed in length. Sequences obtained directly were on average about 350 bp long and for 95% of the clones both the SP6 and T7 end-sequences were obtained at the first attempt. Sequences obtained by DOP-PCR were mostly shorter than 300 bp. For 40% of the BACs we obtained only very short amplicons of 50 to 100 base pairs from one end. In two cases the sequence obtained with the DOP-PCR differed from the sequences obtained by direct sequencing, and in these cases *E.coli* or vector sequences were amplified (data not shown). Taking the advantages and disadvantages of both methods into account, we decided to use direct termini sequencing for the systematic determination of the SP6 and T7 end-sequences.

**Example 3 : Representativity of the library.**

After having determined the end-sequences of 400 BACs a certain redundancy was seen. The majority of clones were represented at least 3 to 4 times. Maximum redundancy was seen in the vicinity of the unique *rrn* operon, as 2.5 % of the clones carried identical fragments that bridge the cosmids Y50 and Y130 (Fig. 3, approximate position at 1440 kb). The majority of clones with identical inserts appeared as two variants, corresponding to both possible orientations of the *Hind*III fragment in pBeloBAC11. This suggests that the redundancy was not the result of amplification during library construction, but due to the limited number of possible combinations of partial *Hind*III fragments in the given size-range of 25 to 120 kb. To detect rare BAC clones, a pooled PCR protocol was used. Primers were designed on the basis of the existing cosmid sequences and used to screen 31 pools of 96 BAC clones. When positive PCR products of the correct size were obtained, smaller subpools (of 8 or 12 clones each) of the corresponding pool were subsequently used to identify the corresponding clone (Figs. 1A and 1B). With this approach 20 additional BACs (Rv401-Rv420) were found for the regions where no BACs were found with the initial systematic sequencing approach. The end-sequences of these BACs

(Rv401-420) were determined by direct sequencing, which confirmed the predicted location of the clones on the chromosome. A 97% coverage of the genome of H37Rv with BAC clones was obtained. Only one region of ~ 150 kb was apparently not represented in the BAC library as screening of all pools with 5 several sets of specific primers did not reveal the corresponding clone. This was probably due to the fact that *Hind*III fragments of mycobacterial DNA larger than 110 kb are very difficult to establish in *E. coli* and that a *Hind*III fragment of ~120 kb is present in this region of the chromosome (data not shown).

**Example 4 : Establishing a BAC map.**

10 Using all end-sequence and shotgun-sequence data from the H37Rv genome sequencing project, most of the BAC clones could then be localized by sequence comparison on the integrated map of the chromosome of *M. tuberculosis* strain H37Rv (Philipp et al., 1996b) and an ordered physical map of the BAC-clones was established. PCR with primers from the termini sequences 15 of selected BACs were used for chromosomal walking and confirmation of overlapping BACs (data not shown). The correct order of BACs on the map was also confirmed more recently, using 40,000 whole genome shotgun reads established at the Sanger Centre. In addition, pulsed-field gel electrophoresis of *Dra*I digests of selected BACs was performed (Fig. 2) in order to see if the 20 approximate fragment size and the presence or absence of *Dra*I cleavage sites in the insert were consistent with the location of the BACs on the physical map (Fig. 3). Comparison of the sequence-based BAC-map with the physical and genetic map, established by PFGE and hybridization experiments (Philipp et al., 1996b), showed that the two maps were in good agreement. The positions of 25 8 genetic markers previously shown on the physical and genetic map were directly confirmed by BAC-end-sequence data (Table 2, Fig. 3). The position of 43 from 47 Y-clones (91%) shown on the physical and genetic map, which were later shotgun sequenced, was confirmed by the BAC end-sequences and shotgun sequence data. Four clones (Y63, Y180, Y251, and Y253) were located to 30 different positions than previously thought and this was found to be due to book keeping errors or to chimeric inserts. Their present approximate location relative to the *oriC* is shown in Figure 3: Y63 at 380 kb, Y63A at 2300 kb, Y180 at 2160 kb, Y251 at 100 kb, and Y253 at 2700 kb. A total of 48 BACs, covering 35 regions of the chromosome, not represented by cosmids were then shotgun sequenced (Cole et al., 1997), and these are squared in Fig. 3. No chimeric BACs

were found, which is consistent with the observations of other research groups for other BAC libraries (Cai et al., 1995; Zimmer et al., 1997). The absence of chimeric BACs was of particular importance for the correct assembly of the *M. tuberculosis* H37Rv sequence. The exact position of the BAC termini sequences 5 on the chromosome will be available via the world wide web (<http://www.pasteur.fr/MycDB>).

Table 2 : Identities of genetic markers previously shown on the integrated and genetic map of H37Rv (Phlipp et al., 1996b) which showed perfect sequence 10 homology with BAC end sequences.

Locus	BAC end sequence	Description of genetic marker	Organism	GenBank Accession n°
<i>apa</i>	Rv163SP6	Secreted alanine-proline-rich antigen	<i>M. tuberculosis</i>	X80268
<i>dnaJ, dnaK</i>	Rv164T7	DnaJ hsp	<i>M. leprae</i>	M95576
<i>fop-A</i>	Rv136T7	Fibronectin binding protein	<i>M. tuberculosis</i>	M27016
<i>polA</i>	Rv401T7	DNA polymerase I	<i>M. tuberculosis</i>	L11920
<i>ponA</i>	Rv273T7	Penicillin binding protein	<i>M. leprae</i>	S82044
<i>pslC</i>	Rv103T7	Putative phosphate transport receptor	<i>M. tuberculosis</i>	Z48057
<i>recA</i>	Rv415SP6	Homologous recombination	<i>M. tuberculosis</i>	X58485
<i>wag9</i>	Rv35SP6	35-kDa antigen	<i>M. tuberculosis</i>	M69187

#### Example 5 : Repetitive end-sequences.

Repetitive sequences can seriously confound mapping and sequence 15 assembly. In the case of the BAC end-sequences, no particular problems with repetitive sequences were observed. Although nine clones with one end in an *IS1081* (Collins et al., 1991) sequence were identified, it was possible to correctly locate their position on the map using the sequence of the second terminus. Moreover, these BACs were used to determine the exact locations of 20 *IS1081* sequences on the map. Five copies of this insertion sequence, which

5 harbors a *Hind*III cleavage site, were mapped on the previous physical and genetic map. In contrast, BAC end-sequence data revealed an additional copy of *IS1081* on the *M. tuberculosis* H37Rv chromosome. The additional copy was identified by six clones (Rv27, Rv118, Rv142, Rv160, Rv190, Rv371) which harbored an identical fragment linking Y50 to I364 (Fig. 3, at ~ 1380 kb). This copy of *IS1081* was not found by previous hybridization experiments probably because it is located near another copy of *IS1081*, localized on the same *Dra*I fragment Z7 and *Asn*I fragment U (Fig. 3, at ~ 1140 kb). Furthermore, the position of a copy of *IS1081* previously shown in *Dra*I fragment Y1 (Fig. 3, at 10 ~ 1840 kb) had to be changed to the region of Y349 (Fig. 3, at ~ 3340 kb) according to the end-sequences of BAC Rv223. The positions of the four other *IS1081* copies were confirmed by the sequence data and therefore remained unchanged. In total 6 copies of *IS1081* were identified in the H37Rv genome in agreement with the findings of others (Collins et al., 1991).

15 In addition, a sequence of 1165 bp in length containing a *Hind*III site was found in two copies in the genome of H37Rv in different regions. The end-sequences of BAC clones Rv48 and Rv374, covering cosmid Y164, as well as Rv419 and Rv45, that cover cosmid Y92, had perfect identity with the corresponding parts of this 1165 bp sequence (Fig. 3, at ~ 3480 kb and ~ 900 kb).  
20 Analysis of the sequence did not reveal any homology with insertion sequences or other repetitive elements. However, as each of the two locations showed appropriate BAC coverage, chimerism of the sequenced cosmids Y164 and Y92 can be ruled out as the probable cause.

#### **Example 6 : Using BAC clones in comparative genomics.**

25 The minimal overlapping set of BAC clones represents a powerful tool for comparative genomics. For example, with each BAC clone containing on average an insert of 70 kb, it should be possible to cover a 1Mb section of the chromosome with 15 BAC clones. Restriction digests of overlapping clones can then be blotted to membranes, and probed with radiolabelled total genomic DNA from, for example, *M. bovis* BCG Pasteur. Restriction fragments that fail to hybridize with the *M. bovis* BCG Pasteur DNA must be absent from its genome, hence identifying polymorphic regions between *M. bovis* BCG Pasteur and *M. tuberculosis* H37Rv. The results of such an analysis with clone Rv58 (Fig. 3, at 30 ~1680 kb) are shown here. This clone covers a previously described polymorphic genomic region between *M. tuberculosis* and *M. bovis* BCG strains (Philipp et 35

al., 1996a). *EcoRI* and *PvuII* digests from clone Rv58, fixed on nitrocellulose membranes, were hybridized with  $^{32}\text{P}$ -labelled total genomic DNA from *M. tuberculosis* H37Rv, *M. bovis* (ATCC 19120), and *M. bovis* BCG Pasteur. Figures 4A and 4B present the results of this analysis, where it is clear that 5 several restriction fragments from clone Rv58 failed to hybridize with genomic DNA from either *M. bovis* or *M. bovis* BCG Pasteur. On the basis of the various missing restriction fragments, a restriction map of the polymorphic region was established and compared to the H37Rv sequence data. The localization of the polymorphism could therefore be estimated, and appropriate oligonucleotide 10 primers (Table 1) were selected for the amplification and sequencing of the corresponding region in *M. bovis*. The alignment of *M. bovis* and *M. tuberculosis* H37Rv sequences showed that 12,732 bp were absent from the chromosomal region of the *M. bovis* type strain and *M. bovis* BCG Pasteur strain. The G+C content of the polymorphic region is 62.3 mol%, which is the same as the average 15 genome G+C content of the *M. tuberculosis* genome, hence indicating that this region is not a prophage or other such insertion. Subsequent PCR studies revealed that this segment was also absent from the Danish, Russian, and Glaxo substrains of *M. bovis* BCG, suggesting that this polymorphism can be used to 20 distinguish *M. bovis* from *M. tuberculosis*. Analysis of this sequence showed that 11 putative open reading frames (ORFs) are present in *M. tuberculosis*, corresponding to ORFs MTCY277.28 to MTCY277.38 / accession number Z79701 -EMBL Nucleotide Sequence Data Library (Fig. 5). FASTA searches against the protein and nucleic acid databases revealed that the genes of this 25 region may be involved in polysaccharide biosynthesis. Among these putative genes, the highest score was seen with ORF 6 (MTCY277.33), whose putative product shows a 51.9% identity with GDP-D-Mannose dehydratase from *Pseudomonas aeruginosa* (accession number U18320 - EMBL Nucleotide Sequence Data Library) in a 320 amino acid overlap. The novel *M. bovis* sequence of the polymorphic region was deposited under accession number 30 AJ003103 in the EMBL Nucleotide Sequence Data Library.

As it appears from the teachings of the specification, the invention is not limited in scope to one or several of the above detailed embodiments; the present invention also embraces all the alternatives that can be performed by one skilled in the same technical field, without deviating from the subject or from the scope 35 of the instant invention.

**Table 3** : End-sequences of the polynucleotide inserts cloned in the named recombinant BAC vectors contained in the I-1945 *M. tuberculosis* H37Rv genomic DNA library.

RvXXXSP6 corresponds to the SP6 end-sequence of the clone RvXXX.

RvXXXT7 corresponds to the T7 end-sequence of the clone RvXXX.

RvXXXIS 1081 corresponds to a region located close to a copy of the IS1081 repetitive sequence (Insertion element).

The character « - » denotes an uncertain base residue.

Clone Rv101

:::::::Rv101SP6.seq:::::::  
 AATACTCAAGCTGCCAGCCGTCGATGACAAGAAATATGTCGCAGGGCGACTTGTCTCGCAGCTGCGGTACCGCGCACCAGTCTATGCCGTGGTCGCGGAAATGCCCTCCGAAATCGCACGGCGACTCCAGTTCGGC  
 GAGCATCCCGCATGCCAGCTCGCGCTGCCCGCCACGGCACCCACATGCCAGTTCGTCCACCTGGGCCAGCGCCCCCGCCGAATTCCAAACAATAGAACTGCACCCGGCCCGCATGTGGGTAACAGCCAACGCCATGATCAGCGT  
 CCGCAGCGCGTTGACTTGGCCGTTGCGGTGCACCTACGAACGCGACATTGCCCTGCCGGCCCCGACAAGTCGATCGTGGGACCGGACCCGTGACTGCTAACGGCGATTGAAATTCCGAT

:::::::Rv101T7.seq:::::::

CCACCCGTGTAATTGGGATGGGCAAAAGGGCGAACGCCGCGTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGGTTAGGGCTCTCGCGGGAAAGGCCGAAACGTACGGCGTTCAACACCTCGCGTCGCCCTCCGACCGCGAACATTCGGGG  
 ATGGCAGCAACCTGCTGGCACCCCTGGCCGGCGATGATCTGCAGCGTCGCCCGCGGGTAGTCGCCGCCGGCGCTACACTCTGAAACCGCATGACCGATGTGGATGCAGCATCCGACGCAACGGTTCCACCCCGATATGTTCGCCTCGCTGCCCGTGGGACCGGT

Clone Rv102

:::::::Rv102SP6.seq:::::::  
 AATACTCAAGCTTCCGCCATACCGCCATGTCGCGCACATCCAGGACTTCTGGGGGATCCGCTGACAGCGCGGGATCCCAAAGTCCGCGGATGTCGCGCACATGGTGGACACCACACCACGGCACGGGGTAGTCACCGGTCCGGCAGC  
 GGTCCACCGCGGTGCGGCACATGGTGGACACCACACCACGGCACGGGGTAGTCACCGGTCCGGCAGCAGGACTATCGCTAACGGTACCCGCGATCACCAACATGGTACCGCAGC  
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:::::::Rv102T7.seq:::::::

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 ACGGCCAAGGCCGCGTAGCCGACCGTAGGTGCGCCGGCAGGACAGGTGGTAGTCGCCGCGGATCGGCCAGAC  
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Clone Rv103

:::::::Rv103SP6.seq:::::::  
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 CAGGCCGATCAAGCCTTCGCCGAGGCCAAATTCCAAATCAAGAGGCCAAGGCCGTACCAATCAGCCGGCAACGAGGGATTC  
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:::::::Rv103T7.seq:::::::

TGCTCCCGAAACCTGGGGGTGTGCCTGCTCTGTATGCAACGGCATACGGACATCCTTCCCTGAGACCCGCGGTGCAAC  
 CAGCCACGTGTCATCATAGNGGGCAACCCCGGCCAAGGGCGACGGCACGCCAAGTTCGCCGACCGTTAACCTAGTG  
 CTGTTAGCTTCATTGCTGCCGATCAAACAGCTGGCGGCCGTTAGGAACGTGAATTGAAACTCAACCGATTTGGTGCG  
 GCCGTAGGTGCTGGCTGCCGGTGCCTGGTGTGGTGTGGTAACGACGACAATGTGACCGGGGGAGGTGCA  
 ACCACTGCCAGGCCGTCGGCAAAGGTGCGATTGCCGGGGAGAAGACACTCAAAGCCAGTGGT

## Clone Rv104

:::::::Rv104SP6.seq:::::::  
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 GCGGAGCGTCTGCTGATTCCGATCACGTCGGCGCTCGCATCGAGCATGGCGCCGGCAGCGTAGCAGCGATCCGCC  
 GTCGTGAGGAGCACGACACGAGCGTACGCCCCGCCGTAAGCCGCGCCAGGATTGGCGAAAAACCGTTCTACGTG  
 GC3GGTGTACTGGGTGTCGAATGATTGGGTGCGTAGGGCTGCTGCAATCGTCGACATAGATGCCGTCGGCG  
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TCCTATGTCCTGCCGAGCAGTATCGAACCGCGTACAGAGATTGTCTATCCTGGACCTGACGGTGAGGTCGAAGTT  
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 ATATACGCTTCGGGTTACAGAGATGTCGATGGGGCGCTGGAGGCTTCACGTCCATGGGCCACAAAGGATGTTGTCGG  
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## Clone Rv105

:::::::Rv105SP6.seq:::::::  
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 GAGCTACATCAGCTCGGCCGCCAGTGGTCGGCCCTCTTCAGGTCGAAGTCTATACCGATATGCGCATCCGCAGC  
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## :::::::Rv105T7.seq:::::::

GGTACGCTTCGGTCGAGTCTGCGAGTGTGATGACGACGGGACCTCGTCGGCATCTTCATAGCCGCCACACCT  
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 GGTCAAGGCCCTCGGGTCCGGCCAGCACTCCGCAAGCTTCGTCGGGTGGTCGCGACGCGCATGGGCCACCATCGCAT  
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 CGGGAAACATGTCACGGTAGGTGGTACCGGCTACCGGCTGA

## Clone Rv106

:::::::Rv106SP6.seq:::::::  
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 GCGGC

## :::::::Rv106T7.seq:::::::

GGCTNGCGTACCCGGTACCGGCCGCGGGCTTACACACGTGCCGAACGGAACTGGAAGCGCAGTAAGCCCTAACGCCAACCG  
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 CGATCCGATGCCCTCCAGTTGCGTGAGCAANCAGCGGAGTCNTCGGGGATCGATGCCACGGGTGTTCAATGG  
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## Clone Rv107

:::::::Rv107T7D4.seq:::::::  
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 GGACACNANAGTATCNCAGTCACCGCGATCACGAGCATGGTATCGNNCAATGTTNCTANTGATCTACGCTCCG  
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 ATGTCGCCGTACACAATCNCGCCACGCCGAAGACNGGAAACGCTTCTACACAATNTCNCGGACGCCACTNAA  
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## Clone Rv108

:::::::Rv108T7D4.seq:::::::  
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## Clone Rv109

:::::::Rv109SP6.seq:::::::  
 AACAGCTATGACCATGNTTACGCCAAGCTATTAGGTAACACTATANAATACTCAAGCTTTACGGTATCGGCATC  
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 AGTCCCCTACGTAACCCCTCCGCACTGTCATGGACAACAGCGCCTCTCCACGGACCGGGCCGGGTGTGGGGTGT  
 TTCGGCAGCCAGGTGGTCCACACTGCCGACGGCGCGAGCCGGTACCCGACCAAGCCGGAAACAAGT  
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:::::::Rv109T7.seq:::::::  
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 ACNGAAATACGCAAGATGCCNTCNAGCNGTGTGCGCGGATTATCANGACTGACCTCTGGCTGACCGNNNTGNTG  
 GTCGCGATGCCCTGGCGCCGGCGGTGNTCGTGGCTGGATAGCGAAGTCAGCTAATTCTCGTGGCAGCTCG  
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## Clone Rv10

:::::::Rv10SP6D2.seq:::::::  
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## :::::::Rv10T7D4.seq:::::::

NCCGTCGTTGACAAGTAAATATGTCGCAAAAGTCTAGCGGCGACTTTGCTCGCAGGTGGCGTACCGCGCACCG  
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## Clone Rv110

:::::::Rv110SP6.seq:::::::  
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 CTCCACCCANCCAGCAGGCAGCGCAAGCTGAATCTCAACCGGGTTGTCNATCGGACAAGTTGGGGTGCCTTGG  
 GGCAATGACAGGGTGGCNGCGGTGCGTTGGTCCGGCGGGGAAGTGCTGCGTGGGATCNCCTGGCTGGCATTGGC  
 NTTTTGCGCGGGCCGGTGGTNGGGGGCAACAGGTNTCCCNGTGCGGGTGGCGCTAACGGTCNACGGCGAACCG  
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## :::::::Rv110T7.seq:::::::

CTACACCATCGAACGACGGCGTCGCCNACTTCCCGGTACCGCTCAACTTGTGTCACCCCTAACGCCATTGC  
 CGGCACCTACTACGTGCACTCAACTACTCATCCTGACGCCGAACAAATTGACGCAAGCGGTTCCGCTGACCAATAC  
 GGTCGGTCCCACGATGACCCAGTACTACATCATTGGCACGGANAACCTGCCGCTGCTAGAGCCACTGCGATGGTGC  
 GATCGGGGAACCCACTGGCAACCTGGTTCAACCAAACCTGAANGTGATTGTTAACCTGGCTACNGCACCAGG  
 CTATGGTTATTCAACCTCNCGCCAATGTTGCGACTCGTGGTGGTGTCCANAGTCNNCCGGTGTACATCGC  
 CGAACACTCTCNCGCCAACAGGAATCNGCNATTCCNCTACAAATCANCACCTCCA

## Clone Rv111

:::::::Rv111T7.seq:::::::  
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 CGACGGTGGCGGTGCGAGCGAAGGTGACGACTGATTGATCGAGTCCAGGTCCAGCGGGTGGCGACCAACG  
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## Clone Rv112

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 CAACCTGCGGTGCCAGGCCATTGACGATGTCGCTGGCGCCCGAGTCCGCGCACCACGACGCCGGCG  
 ACCANGGCGGCCACCCCTGCACGGCGACGATCATCCGGCGCCGTCACGGCGGGGGCTCGAACANGCACAGCA  
 TCAACGTNGTCAACCGGCCGTGACCGGGCCGATCGTACACACCAAGCCATTGCGCTCTCCCAACNGGCGA  
 CCCGGCCCGATCGTACACGGNCTAAGGCCATTGGCGCTCT

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TCGGCGCCATCGGCACCTTGGAGGACCTGTATTCGACGCCGTGCCNACCTGAGGTTGGCGGTGGACNAAGTGTGCA  
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NGCTTCTGCTGCTGCGACACCCACNACGTTGGCACCAGCAGCTTAGCTGGCATGCTCTGACCGCGCTGGCGA  
CNACTCCAGACNTTCAANAGTGGTGCCTNNCCAAATGTNCCGNANTGTCTCGGNNTCCCTTACCNCCAAATGGGCN  
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Clone Rv113

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AAAACCNCGTTCCATATCCCGCGACGAAAAGAACGCCAGTTCCGCTACTTAACCCCTCCCGGAACCGTCCATGGACAA  
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|||||||||:Rv113T7.seq|||||||||

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GTCGGCGACCGTCGTCATGGTCGACACCCACGACGGAAAGACGCAAGATCGCGTCAAGCATGTGTGCCGGATTATC  
AGGACTGACCTCCTGGCTGACGGGATGTTGGTCGCGATGCCCTGGCGCCGGCGTGGTCGTGGTCGGCTCGGA  
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Clone Rv114

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TTGATCAAGGCACCCCTGGTCACCGTGGATCGGGTGGAAAGTTCGACATCTTGGCCACCTGGCGCGGGCG  
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:::::::::::::Rv114T7.seq::::::::::::

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GCCAGGTCTCAAGGAAACGCCCTACGGGGTCAACCGAAGTACGGCCCTTGACCGCGACCGCTTCAACG  
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AATCGCGTTGACGACCAGCGTCGCCAACGCTTCGCCCTCCACGCTTCA  
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Clone Rv115

:::::::Rv115SP6.seq:::::::

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GGANATTNCCTGTTGATGCTGGGATTGCCACGCCAACGGCATCTANCGATTACTCTCCNCGGGGTGGAAAAGTGC  
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GTCNTCAGCGCGCCCACATGGGGTGCCTACGGCACGGCAGGTATGCCGCAGCAACCCGAGCGCGTGGTCATGCC  
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Clone Rv116

Rv116SP6.seq

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AGCATCCGAATGCCAGCTGCCGTGCCCCCTGCCGGCACGGCACCCACTTGCAGCATTGCGTCCACCTGGGCCAGC  
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:::::::Rv116T7.seq:::::::  
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 ATGGCAGCAACCTGGTAGCACCTGGCCGGCGATGATCTGCAGCGTCGCCCGGGTAGTCGCCGCCGGCGCTAC  
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Clone Rv117

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:::::::Rv117T7D4.seq:::::::

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 ACATCATTGCAACGGAGAACCTGCGCTGCTAGAGGCACTGCGATCGTGGGATCGTGGGAACCAACTGGCGAAC  
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Clone Rv118

:::::::Rv118SP6.seq:::::::  
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:::::::Rv118T7.seq:::::::

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 TCAAGTCCGGTCTACGCTTGGGCTTGGGACGGTCCCGACGCTGGTGCCTGGCGCTGCCGCGAAAGCGCGGGTCG  
 GTGCCATCAGGAATGCCTCACCGCCGCGCACTGCACGGCACTGCGCCAGTGCCTGGCGATGTCAGCCATCGGACATCATGCT  
 CGCGTTCAACTCCTGACCAGTCGGCGAACAGCTCGATTCCGGACCGCCAGCGCATTGGTGTGGAAATCGCGA  
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 ATC

Clone Rv119

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 CAGACGCCGCTTCGGACCCCTGCTGTCACCACAGTGGCAACGCTTAAATCACCGCAAGCTTGGGAATCCA  
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:::::::Rv119T7.seq:::::::

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 TGTACTCGTTGGGGCTTGCACCCGGATCGCGGTGGTGCACCATGCGTTGGCTGACGGTGTG  
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 CTACCAAGCGGCA

Clone Rv11

:::::::Rv11SP6.seq:::::::  
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:::::::Rv11T7.seq:::::::  
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Clone Rv120

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:::::::Rv120T7.seq:::::::

GCTCTACGCCGCTACGGTCGAACATGCATCCCGAGCAGATGCTCGAGCGCACCACACTGCCGATGGCCGAAAC  
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Clone Rv121

:::::::Rv121SP6.seq:::::::  
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:::::::Rv121T7.seq:::::::

CCACGGCGTGGATCAAGGTACCGGCCGGATGTTGGCGCAATGGCAGGTTGTCGCGCTTGATGTCGGCGTTAGCGC  
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 ACGCAATCCGTGCGGTACGGTCGGGTACTCGATGTGCGCAGCTTGGCGTTGACACCATCTTGTCAATTGCGGC  
 GAAAGTCGATCATCCGTAAGCGCCTATGACCGCCCTTGTGCCGGTGTAAATCCGCCATGCGCGTTGCGTC  
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Clone Rv122

:::::::Rv122SP6D2.seq:::::::  
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 CCTCGGACTAGCACGGCGGCCACTAGGAAGTACAAGAANGGCCACACCGATGCCGGTAAGGCTGA  
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Clone Rv

:::::::Rv123SP6D2.seq:::::::  
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:::::::Rv123T7D4.seq:::::::

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 GCCGGATTGAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGAGTGGTGACGGCTGCCGGCATGGTGTGCGC  
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Clone Rv124

:::::::Rv124SP6D2.seq:::::::  
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ACGGCCGATGAGCTGACCGAGGTGACAGCGCCGTGTTGGCTGACTTGGAACCGACATGGAGTCGCCCGGTTGGCGT  
CACCTCAAGCATTCAATGGTTATGCGACCAGTTGGGTTACGCCGTACGACATCACGTCGGAGACTTGGATGAGC  
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:::::::::::::::Rv124T7D4.seq:::::::::::::  
CGGGTTGCGGATCCACGCGTGCGGGTTGTCAGCAGCTACGGCACTGAACCGCGCCACAGCTCGCCGATCCGCTTTCG  
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Clone Rv126

:::::::::::::::Rv126SP6.seq:::::::::::::  
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GATGTCGGTATCCTGCTCTGGCGGTGGACTACAATCTGCTGCTGATTTCGGTTGAAAAGGAAATTGG  
GGCGGATTGAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGGAGTGGTGACGGCTGCCGCATGGTGT

:::::::::::::::Rv126T7.seq:::::::::::::  
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Clone Rv127

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Clone Rv128

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Clone Rv129

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Clone Rv130

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Clone Rv132

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Clone Rv134

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## Clone Rv135

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## Clone Rv136

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## Clone Rv137

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## Clone Rv138

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Clone Rv139

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Clone Rv13

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Clone Rv140

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Clone Rv141

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Clone Rv142

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Clone Rv143

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Clone Rv144

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## Clone Rv145

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## Clone Rv146

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## Clone Rv147

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## Clone Rv148

:::::::::::::Rv148SP6.seq:::::::::::::  
 ATACTCAAGCTTCCGCCGATACCCGCCATGTCGCCACATCCAGAACTTCTGGGGGATCCGCTGACAGCGGGGGA  
 TCCCAAAGTGCAGGATGATCGGGCGCCTACGTCGGGTGATCTCGGGTAACAACGAAACCGAAGCGTATGACTCG  
 GTCCACCGGGTGCAGGACATGGTGGACACCACACCGCCACCGCACGGGGTGAAGGCTATGTCACCGTCCGGCAGCA  
 CTCAATGCCGACCGAGGCCGAGGCCGGAGACAAAAGTATCGCTAACGGTACCCGATCAGGAGCATGGTATCGCAGCA  
 ATGTTGCTAGTGTATCGCCCGTAATTACCGGGTCTCGTCTGATCATGGTGGCATCGACCTCGGCCAATC  
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 CGATTGCNGCGAAC

:::::::::::::Rv148T7.seq:::::::::::::  
 CAGGCATGCAAGCTTGGCGTGCCTTCAACCCGAATTGGCTTCGGGCCATCGGTGAGGACGGCGTGCCTGGCTC  
 AACGACGACGCTCGCTGGACACACCTCGATGCTGCCCATGGACGCGTGAACGCAAGCAGCTGATCGAGCTA  
 CAACGCCGCGCGAACGCTTCCGCCGCGGTGACCGCATCCGTTGACCGGGCGATCGCGGTATCGTCGATGAC  
 GGCATGCCACCGGAGCGACGGCAAGCGGGCGTGCACGGTGCACGGGACAAGGTGGTGTGGCGACCCGGCG  
 GTCCCCATGGCCAGACGACATCGTGGCAGATTGCCGGTACGCCGATGAAAGTGGTGTGGCGACCCGGCG  
 TTGTT

## Clone Rv149

:::::::Rv149SP6.seq:::::::  
 ATACTCAAGCTTGGCATTGTGCACATTCCACCGTGCCTATTAAATGCTGAGCCGTAATTGTGACCCAGTCGG  
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 TGGACAATCGTCGCTGTAGCGCTCGGAACACCTCAGCTTCTGCTGCCGCGGCTTCTCCGGCGATGGTAACCCCA  
 GGTTTCGCCACGGCTTACGTAGCAGTGCAGCGGTGTTCATCTCATCGACCTGTTGACTCATCCTGTCAAGGAT  
 GAAGGGTACTGGGCCACTGCGCCTCTGCCGCGCAGGTCGGAATCACCAGGATCTCAGAAACGAGCTGCGACTC  
 ACTCTCCAGGCCACCCGGCGAAAGCTCGACATGGTCAATCCGGCG

:::::::Rv149T7.seq:::::::  
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 GCCGGTCAAGGTGCCCTTCCAGTCACGCCGCTGTGGTCCGGGAACCGCTTATCTTCAATCGAGACGATGCCAGCTT  
 CATCGTGTGGCGATCTGTCGAGGGCACCTCGAACCGGGCGCTCGGAGTACAGCCACCGGATCGTGTGTTGCCCTTCGC  
 GTCGACCATCGTCGATACCGCAGGCACTGGCC

## Clone Rv14

:::::::Rv14SP6.seq:::::::  
 ATACTCAAGCTCCGGCGCCAGTACCGAAAGCGCGAACAGCTCGCGGAGCCACGACGTGCTCGTGGATTGCC  
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 GTGCCCGGGTCTGGTGCACCTGCCGATCGCACAGGTTGGCCACAACCGGGCGCTTGATGCCGGTCCGCAAGCCC  
 GGCAGTTGCCAAACCCAGCGTGTACGGCTCGGCTCGGAGTTGGCGAAGAAGTGGCTCGGCTGATCACCTACCATC  
 GCCAGGATCTCGTGTACACACGCTCGCCAAGGAGGTTGTTGCTATCGACGGCTTGTAGCCAGATGTT  
 GGAATCGACTATCCGATAGTGTCCGCGCAATGGACTTGTACGCCG

:::::::Rv14T7.seq:::::::  
 AGCTTCGGTGTAGCCGATCACCGGAAGCGCGATGATCACGCCACGTTTCGCCGCCGCCATACGGCGGCTACCGAT  
 CTCCCGCTCATACACCCGCGGTAAATGCCGACGGTGGCTCGGAGCGAAGGTGACGACGCTGATTGAATCGAG  
 TTCCAGGTCCAGCGGGTGGCGCAGCAACGGCGCGAGCTCAACGACGTCAATCACGTTGTCGCTTCTACGGTACCGA  
 CCCGGTACCGTAGTCGCCGGTGCCTGGCGAGAAGTTGACCGCCACCGCGACACCGTCTTGACCGGAC  
 GCCACCCCGGATCGGTTGTTGGCCAAGGTAATTGGTCATTCAATTGACGGACGCCACCCGAGCCCCAGTAC  
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## Clone Rv15

:::::::Rv150SP6.seq:::::::  
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 ACCCGGATCTCGAGGATCACAGCGTTACCCCGGAGCGCGACACCGACAATTCCGACACGCCACGCCATCCGG  
 CCCTGGCCAGCTGATTGGAGCTGGCG

:::::::Rv150T7.seq:::::::  
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 GGCCACTTGTCTACCGGTTACCGAAGATCTTCCGGTACCTGCCGCCGCCAGCTGGCCAGTGGCCAGTGGCC  
 GTTGGCCGCCGCGACGATCTTGGCGTCCACGGTGGTCCGGCTTAGCACGATCCCGAGTCGCC  
 TCACCCGGGT

## Clone Rv151

:::::::Rv151SP6.seq:::::::  
 ATACTCAAGCTTCCAAGTCCAAAGTGTGATCATGCCAAAGAGCTCGACAAAGCCGTAGAGGCCTTGGACCCGC  
 CCGCTCGATGCCGCCGTATACTTCTCGCCGCCAGGCCCTGGTCTCAAGGTGCCGAGGCAGGCCGCTCGTC  
 GGGGTGCAACCTTGATGCCACCGCGCTAACGCCGAGGGTACCGAAAGATCTGGCATCCAGGTACCTCCGCC  
 GAAGACGGGCCGCTGGCTGGCGTCTCCCGGACCTGGTCCGCCGCGCTGTCCGGGTCGCCGCTGGTCACCGAC  
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:::::::Rv151T7.seq:::::::  
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 AGCGAAATCGAGAGCAGGAGGACGAGGTACGAAGCTGCCAGCCGCTACCGCTAGGGCGGATGTCGCCGGTC  
 CGCCACCCGCGTACCGGCCGATCGGACACCTGTATGACCGCGGGCGACGTC

## Clone Rv152

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:::::::::::::Rv152SP6.seq::::::::::::
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CTATGTGCACACGGAATCGCCCCGGCACCGCGATCTCGAGGATCACCAGTGCCCGCCCCCTG
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:::::::::::::Rv152T7.seq::::::::::::
GGGATCGAGGAACAGCGCGTGAACTGATAGGTGGGCCGGCTCGAGCAGGCCGGCATTGTTGATGCGTTACC
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GGCGTCCACGGTGGCTGGGTCACTGCCCGAGCAGGATCGCGAGCGGCCGGTCAAGCCGGTGAACCTCGTGGAGAG
CTTGACCCCTGCCGTGGGGAGGCGAACACAGGTCGGTGCATCTCGACCAGGCCGGAACCTCGGGGTGGCGCC
GACGGTGAACAGGTTGCCTGGCACCGCGGGTAGCCGCCGGACTATGCCGATGCCAGGCCGGATCACCGGTGC
GGTCAGTCGGGTCAAGGATGTCGCCCGGGCAGGTGAAGATCCAGCGGGCCGGCTGGACACNGGTGATCTC
GGTCCACCATCGACTTCTGATCA
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## Clone Rv153

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GGTATATGACCTCGGTTCTCGGTGCTACCGCGTGCCTTGTGAGGATGAACTCGGCTTGGAAATTGTCCAGCCGGC
CCAATTCACTGAGCGCAGATTGTAACACATGCCGGCGACATACGCTTCACCGTGGATCTGCTCCACACGGACCG
CCCTGTCGGGATCCTGTCACGGTAAAGGAATTACNTGCNCTCGGTGCC
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:::::::::::::Rv153T7.seq::::::::::::
CCTTCTGCCACCCACACCGTCAACGCCCGCGAAGTCGACGTCGTCCAGGCCATGCCGGCCTCACGGATGGATTGCG
CGCGGAGCTGGTATCGACGCCGTGGCGACCGGAAACCTACCGCAGGCCCTCTACGCCCGCATCTGCCGGAA
CCGTTGTGCTGGGGTGTGCCGACGCCGACATGCCCTGGACATGCCGTGGTCACTTCTCTCACGCCGGTGC
CGCTGAAGTCGTGGTACGGCGATTGCCCTGCCGAAAGCGACTTCCCACGCTGATCGACCTTGACCTGCATGGCC
GGCTGCCGCTGCAGCGTTCTGGCAACGCATCGGCTCGAAGACGTCGAGGAGGGCTTCCACAAGATGCATGGCG
GCAAGGTATTGCGTTCGGTGGTATGTTGATGGCCGCATCGAGCGCTCATACCCACCGG
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## Clone Rv154

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:::::::::::::Rv154SP6.seq::::::::::::
ATACTCAAGCTTGTATTTGATCATCATGATGATCATCACCCGAAGTGTGGTAGCCGCACTGGTTATCGTGGGTACCGT
CGTCTTCCATGGCGCCTTTGGCTTCCGATTGGCTGTCAGGACATTCTGGTATCGAGTTGACTGGAT
GGTGTGGCGATGTCGGTATCGCTGCTCTGGCGTGGGACTACAATCTGCTGCTGATTTCCGGTTGAAAAAA
AGAAATTGGGCCGGATTGAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGAGTGGTACCGCTGCCGCAT
GGTGTGCGCGTTACCA
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:::::::::::::Rv154T7.seq::::::::::::
ATTGNCTTCGGCGCCATCGTGAGGACGGCGTGGGGTGTCAACGACGACGTCGTCCGCCGGACACACCTCGATGCTGCC
CATGGACCGCGTCAACGCAAGCAGCTGATCGAGCTACAACGCCCGCGGAACGCTCCGCCGCCGGCTG
CCGCATCCCCTGACCGGGCGGATCGCGGTGATCGTCACTGACGGCATGCCACCGGAGCGACGCCAACGGCGCGT
CCAGGTGCCCCGGCGCACGGTGCAGGACAAGGTGGTGCCTGGCGTCCGATCGGCCAGACGACATCGTGGCAGATT
CGCCGGGTACGCCGATGAGGTGGTGTGTTGGCGACGCCGGCTGTTCTGCCGTGGGCAGGGTTACCGCAACTT
CACCCAGACCTCCGACGAAGAAGTGGTGGCGTTCTGGATCGTGC
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## Clone Rv155

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:::::::::::::Rv155SP6.seq::::::::::::
ATACTCAAGCTTTCCCGTCCGTCATGCCCAAGCGCGTGAGGCCGAAGCGGCTGGTACGACTCCCTGTTGTGATG
GACCACTCTACCAACTGCCATGTTGGGACGCCGACCGGATGCTGGAGGCCTACACGCCCTGGTGCCTG
GCCACGGCGACCGAGCGGCTGCAACTGGCGCGTGGTACCGGCAATACCTACCGCAGGCCACCCCTGCTGGCAAAG
ATCATCACCACGCTCGACGTGGTAGGCCGGTCAGCGATCTCGGATGGAGCCGGTTGGTACGACTGGTGGAAACAC
CGCCAGCTGGCTTCGAGTCGGCACTTCAGTGACCGGTTCAACCGGCTCGAANAGGCCTACAGATCCTCGAGCCA
ATGGTCAAGGGTGAGCGCCAACGTTTCGGCGATTGGTACCCACCGA
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:::::::::::::Rv155T7.seq::::::::::::
CGGCCACCGGGGCCACTCCGACAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTCCGACTTTC
CGCGGTACCGCTCAACTTGTGTCACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAACTACTTCATCC
TGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTGGTCCACGATGACCCAGTACTACATCATTC
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GCACGGAGAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGAACCCACTGGCGAACCTGGTTCAAC  
CAAACCTGAAGGTATTGTTAACCTGGGCTACGGCACCAGGGCTATGGTTATTCGACCTCGCCGCCCAATGTGCGA  
CTCCGGTCCGGGTTGTTCCCAGAGGTCAAGCCCGTCGTATCGCCGACGCTCTCGTCGCCGGGACCAGCAGGGAAATCGG  
CGATTCGCCTACA

## Clone Rv156

:::::::Rv156SP6.seq:::::::  
ATACTCAAGCTGGGGTGGCGCTGCGGTGCTTGGCGCGTCGGTATCACACCGCCCACGAAATGGGCAC  
AAGAAGGATTGCGTGGAGCGTGGCTGTCAAAATCACCTCGCCAGACCTGCTACGGCACTTACATCGAGCAC  
AACCGTGGCCATCACNTCCGGGTGTCACACCGGAGGACCCGGCGTCGGCGGGTCCGGCGAAACGTTGTGGAGTTC  
CTGCCCCGAGTGTATCGCGGCTTGCCTCGGCCGTTATTGGAGGCCAACGGCTGCGTCGGCTCGCGTCAGC  
CCCTGGAATCCCATGACGTATCTGCGAACGACGTGCNAACNCGTGGTGTATGTCNGTGGTGTGGGTGGC

:::::::Rv156T7.seq:::::::  
TCGCCACCGCACCGCGGAACGCTCAAAGGCACCTACTGGCACCAAGGCCAACACGTCACCCGTGACCTCTGCG  
CCGACCCCGCCCGAGGTCTGGCGTTACCAACCGAACGGCGAGCCGGAGTCTGGTACGCATCGAACAAAGAGCAAG  
GTGCATGGCGGAGTTGTTCCGCCACTCGTCGATGACGGGGTCGATCCATTGAGGTCGCGCCGTCGGTCGAG  
TGGCGGTACACTCCAGGTACTCGACCTCACAGACGAGAGGACTCGATCCATTGAGGTCGACGAAACAGATCTTC  
TGTCCGACGACTACACCACCCAGGCATCGCCGCCGCGATGCCAACCTCGACGCCGTACTGGCCCCGGCG  
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## Clone Rv157

:::::::Rv157SP6.seq:::::::  
ATGAAATAAGAAGAGCACATCCCTCAGTCGGTTATCACTAGCGCTGCCGACCCGTGTAACCGATCATAGCGAG  
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GGAACAACTCCAGGTAGAGGTACACACCGGGATGCCATTGAGTAATAACTGTGACACTCACACCCCTCATCAAT  
GATGACGAACCTACACCCGATATCCGGTCACATGACGAAGGGAAAGAGAAGGGATATCATCTGTGACAAACTGCCCTCA  
AATTGGCTTCTTAA

## Clone Rv159

:::::::Rv159SP6.seq:::::::  
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GACGGTACCGGAGGGCAGCGACAAACACTTATGCACTGGCGACCCGCGAGACGGTGCACACCCATCCGACGG  
CACAAGCTCAGCCGCCGCTTGTCTCGTGGATCGACATTCAACCACTCTGACCGGGCTGGCGAAGGAA  
GCAGAA

:::::::Rv159T7.seq:::::::  
GGTATAGTCGCTGACCGGTGCAAGGTTGACAATGTGGTGCCTCGGCGCTACGTGCCATCGAGACACTGGCGCA  
GGCTATCGCACCGTTATCGCTACGAGCAAATCGGGTATCGGTTCTGAGCATGAGTCGGCGACCGTCGTATGGT  
CGACACCCACGACGGAAAGACGCGAGATCGCGTCAAGCATGTTGCGCGGATTATCAGGACTGACCTCCTGGCTGAC  
CGGCATGTTGGTCGATGCCCTGGCGCCGGCGTGGTGTGGCTGGATAGCGAGGTCAAGCGAATTCTC  
GTGGCAGCTCGAAAGGGTCTGCCGGTGCCTGGTCTTGCACAGATGGCGCAGGTTACGGTGCAGCGGGGTGCGGC  
CCTGGCGGCCCA

## Clone Rv15

:::::::Rv15SP6D2.seq:::::::  
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CCCTNTCTAGA

:::::::Rv15T7.seq:::::::  
CTGTAGCCACCTGTCATCCCCGTACTGCCGACTCTGGTCATCTCGGATCCGCTGACACCCGCTAAGGCTGCTC  
CTCTCGGTGCATTACCTCACCGACGGCGAACNCCCCAGCTTACGACTATCCGGATGACGGCACCTGGTTGCCGGCT  
AACTTCACCGTCAGCTTGGACGGCGCGCTACCGTCGATGGCGCCAGCGGGGCGATGCCGGGCCGACCGATTG  
GTCNTCANCCTGTCGCGTGAACCTTGCCTGACGTACTCGTGGTGGTGTGGCACCCTGCGCATTGAGGGTACTCCGGC  
GTCGGGATGGGTGTCGTCAGCGCCCGACCGGCAAGGCCA

## Clone Rv160

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:::::::::::::Rv160SP6.seq::::::::::::
ATACTCAAGCTTCGCACGCTCGCGCGCGCGTACCGCCCAACAGATCGTCACTGGTGTGCGTCGTCCGC
CTCGCGCACGTGGTCTGTCAACGTTAACGCCGCCACATGTCTGCGGCCGGCAAAACGTGAAAACG
AGCGGGCAGTCGATGACACCGACGGCCGCCATGGGCCAGGGCTGGCAAATTGATCTGTGCGGCCAGT
GCCAGCAGCGTCCGCTCGTACAGGCCGGCCGACGAGTTGAACCGACATGGCAGGCCGTGCGCTGAAGTCCCAC
GGCACACGGGCCGGCTGGCCGGTCAAGTCAAATTGAAAGTACGGAACCGCTGCACCAACCAA
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## :::::::::::::Rv160T7.seq::::::::::::

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ATCGTTCGACCAGCGCTCCATCCGGCGAGTGGATACTCCCAGCAGGTAGCAGGTGCCACCACGCTGGTCAGTGC
CGTTCAGCTCGCTTGCAGCGCTGCAGCAGCCAGTCGGGAAATAGCTGCCCTGGCGCAGCTGGGATCGCAGCTG
ATGGTGTGCGCACGGGTGTCGAAATCACGGTGGCGTAGCCGTTGCGCTGATTGGACCGCTCATCGCTGCGTTGCG
TAGCCGCCCGCACAGGGCGTCGGCTTCAGCCCCATCAAGGCCGGCGATGAACGTCGAGAGCAGCCGCCAGCAGA
TCCGGGCTCGCCTGTGCGAGTTGGTCAGCCAGAAGCTGCTCGGTGTCGATAAGATGANAAGAAGTCATTGCGTTATTT
CCT
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## Clone Rv161

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AATCGAGTTCAGGTCCAGGGGTGGCGCAGCAACGGCGCGAGCTAACNACGTCAATCACGTTGCGCTTACGG
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CGCGGACGCCACCCCCCGGAT
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## :::::::::::::Rv161T7.seq::::::::::::

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GCGCNAACAGCTCGGGCAGCCCACGACGTGCTCGTCGGATTGCCGGCGAGATCAATTCCAGGCAGCTCCCGGA
CAATCGGGCTCTGCTGGCCCCAACGAGGACTCGAGGTACCCGGTGGCGTGGTGCACCTGCCGATCGC
ACAGGTTGGCCCACACCGGCCGTTGATGCCGGTGGCAAGCCGGAGTTGCCAAACCCAGCGTGTACAGGCTCG
GCTCGCAGTTGGCGAAAAAGTGGCTCGCTGATCACCTACCATCGGCCAGGATCTGCGTGCATCACGACGCTCGC
CAAGGAGGTTGTGTTGCTATGACGGCCTTGTAGCCAGATGTTGGAATCGACTATCCGATAGTGTCCGCCAAT
GGACTTGATCGCCGGCGGTGAGCTGGCTGCCGNGT
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## Clone Rv162

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TCCACCGGGTGGCACATGGTGACACCACACGCCACCGCACGGGTGAAGGCCTATGTCACCGGTCCGGCAGCAC
TCAATGCCGACCAAGGCCGAGGCCGAAACAAAAGTATCGCTAAGGTACCGCAGTACGAACATGGTGTACGCAA
TGTTGCTAGTGTACCGCTCCG
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## :::::::::::::Rv162T7.seq::::::::::::

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CCATGAGCACCGCCAGCCGAGCACGAGGCCAAACTCCGCCAGCAGCAGGCCGGTTGGACTTGTGCTGGACAAGGGG
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GAAGCGAGGAGCACATGGCCGCCACCGCAATGTACACGCTGCAAGCAAACCATGAAACCCGGATGGCTATACATCA
CCGCCCATGCCCGGTCAAGCCGGATCGTCGATGACGGCGAGTACTGATTACGTGCCGGTGAATGCCGACCC
CGGGGAGCACTTCCGCAAAACTAACCGGTTGG
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## Clone Rv163

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TAGTCGAAGTGGCGCGCTCAGACTCCACCCAGCCAGCAGGCCGAANCTGAATCCTCCAACCGGGTTGTCNATC
CGGACAGGTTGGGTGCGTTGGGCAATNACAGGTGGCGGGTGCCTCGGGTCCGGCGGAGGTGCTGCNTTG
GGATCCCCGGCTGGGCATTCCGCTGTTGGCGGCCGGTGGTGGGGGGCAACACGTGTCNCCGGTGCAGGGTGGC
CCT
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## :::::::::::::Rv163T7.seq::::::::::::

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CCAAGATCTACACCATCGAATACGACGGCGTCGCCGACTTCCGCCGACCCGCTCAACTTGTCGACCCCTAACG
CCATTGCCGGCACCTACTACGTGCACTCAACTACTCATTGACGCCGAACAANTGACGAGCGGTTCCGCTGA
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CCAATACGGTCGGTCCCACGATGACCCAGTACTACATCATTGGCACGGAGAACCTGCCGCTGCTAGAGCCACTGCGAT  
CGGTGCCGATCGTGGGGANACCCACTGGCAACCTGGTTCAACCAAACCTGAAGGTGATTGTTAACCTGGCTACGG  
CGACCCGGCCTATGGTATTGACCTCGCCGCCAAATGGT

Clone Rv164

:::::::Rv164SP6.seq:::::::  
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ACCTGGCAGTACCTGCCTCTCGTTGACGATCGATCGTCTATGCCGCCGTCCTCGCGGAACAGGCCNCCAGTACATC  
GCCACAGACGGGATCCACCCGCATTCGGCTACGGTGCTCGTTGGTACTAGTCGGTCCCTGGTGACGTGC  
CGGTGATGCGGACCGTCTAGCACTGACCAATGGCCAAATGCGGGC

:::::::Rv164T7.seq:::::::  
CGGGGGGCCTCTTAATAGTGTAGGAAAGAAGCTCTACATATTCAAGGAGGATTACCATGGCTCGTGGTCGGGATCG  
ACCTCGGGACCACCAACTCCGCGTCTCGGTTCTGGAAAGGTGGCGACCCGGTCGTCGCGCAACTCCGAGGGCTCCA  
GGACCACCCCGTCAATTGTCGCGTTCGCCCGCAACGGTGAGGTGCTGGTCTGCCAGCCCGCCAAGAACCCAGGTGA  
CCAACGTCGATCGCACCGTGCCTCGGTCAGCGACACATGGGAGCGACTGGTCCATAGAGATTGACGGCAAGAAAT  
ACACCGGCCGGAGATCAGGCCCGCATCTGATGAAGCTGAAGCGCAGGCCGAGGCTACCTCGGTGAGGACATTA  
CCGACCGCGGTTACGACGCCCGCTACTTCAATGACGCCAGCGTCAGGCCACCAAGGACCCGCCAGATGCCGG  
TCTCACGTGCTGGG

Clone Rv165

:::::::Rv165SP6.seq:::::::  
ATACTCAAGCTTCATAACAGGCCTGTTGGGCGCACCCGGCTCGCCGAGTTCTGCACGCACCGCCTCAAGTGCAGGCC  
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ATGATGCTGACCTGATCGGCCACCCGGCGTTCTGGCGTCTTCGGTTCACTAATCGGGTGTCAAGCGTCTCG  
ACAGCCACCACCCGAGTGGCACCAGCTGCTCCACACGGACCCAGCGATGCCGTACCTCACCCGTCCAGGGTCC  
ACCACGACACGGTGTGACCGCAGCGCAGGCCATTCAACCACCCAGCGGTACCGCCAGGCCAGATGCCACACCGCC  
ACCATCCCCGATGCAAGGCCAGGCCGGAGTAAGA

:::::::Rv165T7.seq:::::::  
CTGGTGTGGACGGAGCTAGTACAACACTCCTCTCAATGCTCTGCCCCGATCGCGCGACCAGGATGACCCAGGAC  
ATCCTGCCGCCGAAGTACTGGAAAGCTCACACCCGAGTTCTCGTCGACCCGGTGGTGGCTACCTGTGCAACCGAGGAG  
TGTGCGACAACCCATGGTGTACGTCAGTGGTGGTTAGGTGCAAGCGAGTTGCGCTGTTGGCAACGACGGCGCC  
AAACTCGACAAACGCCGTNGTACAAGATGTTGGCGCGGTGGCCAGATCNCCGATCTGTCCGGTGCAGAAAATT  
GCTGGATTCAAGTTGAGAACTAAAT

Clone Rv166

:::::::Rv166SP6.seq:::::::  
ATACTCAAGCTTCGGCGTGTCCACCTGACCCAAAAGGCCAGGTGCGCCGCCAACGGCCCGCTGGCCGCC  
ACTGGTCGGCGTCGCCGTGGCGACAATCAGTAGCTGGACATCGGAAACCGCTGCACCACCTCGGCAGCGCGTCAA  
GCAAAACGGCCATTCC

:::::::Rv166T7.seq:::::::  
TTTCAGATCTCATTTTATGACATGACTGGAGATCTGTCTAGATTGCAAGCTCTGTGAGCGTGGTACCGGATTCAAG  
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TTCGCGCACCAAGATCGCGGCCATTGGCCGGCGATGACCGCGATGACCAGCGCGATCCAGGAAAACCGTTCCAACC  
AGTGTGGCGGCCATCCCCG

Clone Rv167

:::::::Rv167SP6.seq:::::::  
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CGCGAGGTGCTGCCAGCCACGGTGCCAACCGCGGCCCTGCCCGCGA

:::::::Rv167T7.seq:::::::  
GTGTGCTGTCAATTCAAGAGCTGAGCCTGATGCACTCAACTTACTGAGCATGCTAACGCTGGTGTGGTCTTGTTC  
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CCAGCTTGGACCGACTTCGATGAGAACGCCCTCTGCCGTATTGAACTGGCGTGCACGGTCGCTGAGCAGCGCTC  
GCCGAGTGGCGCCGCTGATTCTTCATCGAGCCAGGGCGCATTCGTGTTCCGGCCGCTGCGGGTCGGCCCCATCGT  
CGACGCGATCCGTCACCCACTCCTCGATCAGGTCTGCCATCGAACGGGCAACGGTGTGTCGGAGATATGTGTGCG  
TGGGCACGGCGAGCCGGGTGCTGTTGATACACCACCGTTGCATGACCAAGTTGACGCCGACTGGCTGAGCACCGCGA  
TCGGCTCACAGGTGGAAACGTTGGTG

Clone Rv169

:::::::::::::Rv169SP6.seq:::::::::::::  
ATACTCAAGCTTTGGCTAGCCGGCCGAGCCCGATACAGGTGTCAATTGCCACCGCGGCTGTCGGAAATGG  
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CAGCGCGAAACTGAATCCTCCAACCGGGTTGTCGATCCGACAGGTTGGGGTGCCTTGGGCAATGACAGGTGGCGG  
CGGTGCGTCCGGGTCGGCCGGCGGAAGTGTGCGTTGGGATGCCCGGCTGGCATTCTGCGTGTGGCGGGCGGGCGG  
TGGTGGGGGGGCAACAGGTGTCTCCGGTGCGGGTGGCGCTGCACC

:::::::::::::Rv169T7.seq:::::::::::::  
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CCGCTCAACTTTGTGTCGACCCCTAACGCCATTGCCGGCACCTACTACGTGCACTCCAACTAACCTCATCCTGACGCCG  
GAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTGGTCCACGATGACCCAGTACTACATCATTGCGACGGAG  
AACCTGCGCTGCTAGGCCACTGCGATCGGTGCCGATCGTGGGAACCCACTGGCGAACCTGGTTCAACCAAACATTG  
AAGGTGATTGTTAACCTGGCTACGGCGACCCGGCTATGGTTATTCGACCTCGCCGCCAATGTTGGGACTCCGTTG  
GGGTGTTCCCAGAGGTCAAGCCGGTCGTATCGCCGACGCTCTCGTCGCCGGGACCCAGCACGGAAT

Clone Rv16

:::::::::::::Rv16SP6.seq:::::::::::::  
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CACCAAGGGCCCCACACGTACCCGTGACCTCCTGCGCCGACCCGCCGAGGTCTGGCGTTACCACTGAACGGGC  
GAGCCGGGGAGTCTGGTACGCATCGAACAAAGAGCAAGGTGCATGGCGGAGTTGTTCCGCCNTTTTTATGACGGG  
GTCGATCCATTGAGGTCCGTCGCCGCGTCGGTCGAGTGGCGTCACACTCCAGGTACTCGACCTNCAGACGAGAGG  
ACTCGATCCCCTCTANGTGTGGACNAAACAGATCTCTGTCCGACGACTACACACCACCCAGGCCATGCCGCC  
GCGATGCCAACTTCACNCCTGNTGGCCCCGGCGGCGCTCCCCGGTTGTCAAACACCTGCCGTGTTGTTACN  
CACTGCCAACATCNAGCCCAGNCNATCCNAGGTCCGTCACGCCCTCCGCGGCTNCCAACCTNCTCCNCTGATCN  
TCCGCACCAAAACACATGCCGACTCCNTGCNCCNATTGCTTGNATCCCT

:::::::::::::Rv16T7.seq:::::::::::::  
CCGCTATCGGTGGTGTGCTGGCGCGTGGTATCACACCCGCCCACGAAATGGGGCACAAGAAGGATTCGCTGGAG  
CGGTGGCTGTCCAAGATCACCTCGCCAGACCTGCTACGGGACTTCTACATCGAGCACACCCTGGCCATCACGTC  
CGGGTGTCCACACCGGAGGACCCGGCGTGGCGCGGTTGGCGAGACGTTGTTGGAGTTCTGCCCCGAGTGTATC  
GGCGGCTTGCCTGGCCGTTATGGAGGCCAACGGCTGCCTGGCTGGCGTCAGCCCTGGAATCCCATGACG  
TATCTGCCTGCAACGAGCTGCTAACGCGTGGCTGATGTCGGTGGTGTGGGGTGGCTGATCGCGGTCTCGGCCCCG  
GCGCTGATCCCGTTCGTCATCATCCAGGCAGTCTTCGGCTTCAG

Clone Rv170

:::::::::::::Rv170SP6.seq:::::::::::::  
ATACTCATGCTTGCAGATTCGATGGGCGCAGCCAGCGAAGTCGCTAGCGTGGCCGTGTTCTGGCT  
TCGGATCTATCCTCGTACATGACCGGCACCGTGTGACGCTGGCGGCCGTTCATATGACACCGAGATCATTG  
CACGGTACGGCAATTCGTCAAGAAGGAAATCTTCCCAATGCACCGGCCCTCGAACGTGGCAACAGCTACCCGCAAGA  
AATCGTCGATCGGCTGGGTATTGGCTTGCTCGGCGCCGGCTGCAAGGGTATCGACACCACCGAGTTCATCTCC  
GGGCGTGC

:::::::::::::Rv170T7.seq:::::::::::::  
GGCGTCAACGGTGTGGCACCGCGTCTGCAGTTGTAGGCCTGCAGTTGTGCATCAGGCCGATGCCGCGGCCCTC  
GTGGCCACGCATGTACAGCACCGCCGCGCCCTCACGGGCACCATGCCAGCGCGGGTCCAGCTGAGGCCGCA  
ATCGCAGCGGCGTGAACCAAAACATCGCCGGTCAAGCACTCCGAATGCACCCGGACCAGCACGTCGTACCGTCGGC  
GTTGGGGCCGGCGATCTGCCCGGACCAGCGCGACATGTTCCACGTCCTCGTAGATGCTGGTGTAGCCGATGGCGCG  
AATCTCCCAGTACGGAGTCGGAAATCCGCGCCTCGGCG

## Clone Rv171

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:::::::::::::Rv171SP6.seq::::::::::::
ATACTCAAGCTTCGGCCTCGCTGCAGGAGTGGGAGCCGCAGGGCTGGAAATCGAAAAACGAGCCGGTATCGCACTG
TCGCCGATCGGGGCCACCTGGTGGTACCGATGAATCCGACCCAAATGTGGCTCGGGTGGCTTCTGAC
TCCTGGCCTCGACTCTTGTGGCAGCCACCAGCGGGTGGTCCAGGATCTGGATGGGCAAAGTTGTGCGGCCCGGCG
GTGACGCCGATGAGCTGACCGAGGTCGACAGCGCCGTGGCTGACTTGGAACCGACATGGATTGCCCGGGTTGG
CGTCACCTCAAGCATTCAATGGTTAT
```

## :::::::::::::Rv171T7.seq::::::::::::

```
ATCGCTACCCCGATGCGCCCAGATCGGGCTTCGCAAATAAGCACGAACAGGCAGGCAAAACGTCTATCTGGAGC
CGGAAGGGCAATCAGCCGACCGTCGACGAACGACACCAGCATAACCACTTAGGCCTGAACGGCCGCCAAACATT
ACGCCTCCGTTGATAAGGCTTCGGTCTTCCCCGTCATCCCAAGCACCTTGGCAGGAAATTGAACGCTTCTGT
CGGGCACCGGCCCCGGGCTTGGGTCCTCGA
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## Clone Rv172

```
:::::::::::::Rv172SP6.seq::::::::::::
ATACTCAAGCTTCATCGCGCGCCACAATCAAATATCGCTAGCGTCTCGATGAGCGTCGGTCCGCATCGGCTA
GGGGCCGCATCACGTCGGTATCGAGGGCACGATCGCCCAAGGGCTCGCCCATCAAGGGCGCTCGGGCAAAATTC
CCCTATCCAGCACGGGCCGCGCTCCGCNCAGCCGGCAGGGCTTCATCCCGAGATCGCCTCGCTAGCGCTGC
GGTGCGCCGCGGTCAAGCATGGCGCCGTGGGCGATGACCACCGGGCGT
```

## :::::::::::::Rv172T7.seq::::::::::::

```
TTCGGCGGGTCTGTAGATTGGCTCGGCCACCCCACAGGCACTCATGAACCCAGCCCAGATCGATCTGGTGG
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## Clone Rv173

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:::::::::::::Rv173SP6.seq::::::::::::
GCGCACCATGCCAGTAGGTGCCGTGGCGCTCGAGCCACCCGAGCGGAAACCGCAGTCCGAACAGAACAG
CAGGACGGCGCAACCAGGGCGGTGACCATGCCCGCGCTGAACATCAACCACAGGAAGGGCTCGCGAGCGTCC
GCGCAGC
```

## :::::::::::::Rv173T7.seq::::::::::::

```
CATCGCGAACTTCGGTCCGGTTGNTAGNACCGCAGCACCAAACGCACCCACCGACCCCCACGCTCACGCCAACCC
TTTAGTTCAATTGGCTGAACACAGCAGCGTAGCCGGTGGCCGATATATGTGGAAAATGTTGGACGTACAAAAAA
GTTCCCTGACGCTGGCGTCAACTCGAAACTGCCTCGGAAGTCAATGATGATCATCAGTCAGTCATATTAAAGTCG
```

## Clone Rv174

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:::::::::::::Rv174SP6.seq::::::::::::
ATACTCAAGCTTGCTCGCTCAGCGTATGCATCCAACAGCGCATCGCAGTCAGGCAGGCCGATTTCGG
GCCGGGGCAGTGGCACTGGCCAGATGGCGTTTTTCGAGAAAATTCACGCGCTGAGCGCTGCTCCCATCGAGAG
ACCGGTGGCCTCTACAACCGATGCGACAGTGGACCGCGATGTTGCCAGCGCTCACATACGGCAAGTNTGGC
GCGG
```

## :::::::::::::Rv174T7.seq::::::::::::

```
TTGTCCAGGCGGGGAATCGGGCAGGGAGACGACACCTTCGTTGCTCGATCGTCGCAACGGGTAGTTGGCCGCGAC
CACGTTGTTGGGTAGCGCGTGGATGGACGCTGGCCAGTGGCAGGCCCCAGATCCCCAGGCTCAAGCT
CACAGA
```

## Clone Rv175

```
:::::::::::::Rv175SP6.seq::::::::::::
ATACTCATGCTGGCGCTGGTGGCAGCCCACCTGCCACACGGACCGCGTGGACGCCGCTGACGCCCTG
GTGGTCAGCATCGTGGCGGTCTGCTGTGATGCCAATTCGGCCGCAACTGCTGGTGGCGGGTGGTGGCG
CTCGCATTGCTGGCTGGGTGCTGACCCNCGCNCACACCCGGTGGTGGCTGGCTACGGCCTGCTATCGGC
CTGGTGGTCTACGTCCTCGTTGCCGTGGATCGCGAGCTGGTGGGCCCCGGGCTGGTGGCACTGGCAGCAG
TNCGCGCTGTTCCCCGGCATTCGGTCTGTTGCCGTGGTACCCCTGTTGCCGGGTTGGCCC
```

## :::::::::::::Rv175T7.seq::::::::::::

```
CGCCAATTACGATATCGTTAACCGATATCCCGAGCCGATAGCTGGCGGGCTGGGTGGCCAGCGCGCTGCGAC
GAAAGGTGTGACCGTCAAAACAGACACACCACCGGGCGCGTGGCCGCTGTCACCTGCTCGAGATCTCAGCATCCGC
```

AGCCGGTGTGATCGCGTTTGGCGTGTAGTGGTCGCCGCCGACCCGGAAAGGCCGGCCGACACAACCCGGA  
ACAGGAAGTCCGGTACCGCGCCGAAGNACTGATGCGGAACNCGGAGTGCTCAAACGCATCCTGCTGAT

Clone Rv176

:::::::Rv176SP6.seq:::::::  
ATACTCAAGCTTGGGCACTGACTCGGTACCCCTCCGCCCTTGGCAGCAGCACAGCCACAGCGCGTTCGCGGACCGA  
ACGTGGACATCAATAGCCCGAATCGGTGTGCAAGTGGTAAACGGTGTGATCCAGCTTGGCAGCCTTTGCG  
TAGTCTGGGCCACACCCACAGTGCTCGACGGTACGGTACCCATGATGGCCATCAGTGGCATCGGTGAGCT  
GATAATGCCAGCTGGTTGCCAACCCGGTAGCGATCTTGGCGCTGCTGTGACTGATAACCTATCGAGCAAG  
ACAGCCGGTTGCGACAAAATGACTTTGCGATCTTCGGGACTTCGATGGGTGCGTGGG

:::::::Rv176T7.seq:::::::

AAAGTCTGTGCGGGTTCGCTAAACACCCGGCGGACACTCAGACGGTGTGGTGGCGCATGGCACCGCGGGCAGC  
AAAGCGCACTTCTCGGGGGACGACAGCAAGCGACCGCTAGACAAGAGGGTGTGCGCAGGCAGAACGTTGGTACA  
CAGCTGCTGGCGTTCGGGCCACCGATGTTATGCCCGACCGGGTGGCTGCCACCAGACGATGGAGCCACTCGCC  
CGGAACTGAACGTGACCATACACA

Clone Rv177

:::::::Rv177SP6.seq:::::::  
ATACTCAAGCTTGGGTTCCACGCCCGCGCAGCCACGCCGTACCTTCCACCGAGACCTCACCTGCCATCCGAAATGG  
AATCGGCCGTGACGGAATTGGCGCACCGAACACCCAACGAGGTGGCTTCGTCGCAACCGTCAACCGAGTCGCGG  
CCACCGTGCACGGCGACGTTCTACACCCGACCAAGATCCGAAAGCTGCAAGCTCCAGCACCGATCCGACCGTCA  
TCACCGCTGCCGCCGGCACGTCCTGACCTATTGAGCTGGATCGGCCGCTGGTGTGGAGTGCAGGTTAGAAC  
TGGCCTAGAACCGGGGGCACACCGCNCTGGCGGGGAATTCTGACCGCNCCGGCC

:::::::Rv177T7.seq:::::::

CGCGGTTGGCGTAGTTGGACGGGTCGCCCTCGAGGGCAATGATGACGATGACCACGCCATCACGATGGCACCGAG  
AGGGACAACACAGAAAGCTGACGAACTCCCTCTGGCGGCCGGGCTTGTGGTCGCCGATGGCGCAATTACGATCAGGCCA  
TCACGCCGCTCCCCCAGGCCGCGAAGCAGGGTCCCCAGCAGTTGGCGTAGGCGAATTACGATCAGGCCA  
CGCGATAACCTGCCATGCCCTGGGATATCGATGCGGCCAGAACAGGCCAAC

Clone Rv178

:::::::Rv178SP6.seq:::::::  
CCAACAAGAGCATCGGGACATACGGAGTCAACTACCCGGCCAACGGTGATTCTTGGCCGCCGCTGACGGCGCGAACG  
ACGCCAGCGACCACATTGAGCAGATGGCCAGCGCGTGGCGGCCACGAGGTGGTGTGGCTCGCGGCTACTCCCAGGGTG  
CGGCGTGTGACATCGTCACCGCCGCACTGCCCGGCTCGGGTACCGCAGCCGTTGCCGCCCGCAGCGGACG  
ATCACATCGCCGCGATGCCCTGTTGGGATCCCTGGGCCGCGCTGGCGGGCTGATGAGGCCCTGACCCCTCAAT  
TCGGGTTCCAAGACCATCANCCTCTGCAACACGGCGACCGATTGTTCNAGGGCAACCGGTGGCGAGCGCACCTAG  
GCTACGTGCCGGGATGACCAACCAGGCCGCGTTCGTCGCGAGCAGGATCTAACCGCGAGCCGCCATAGATTCC  
CG

:::::::Rv178T7.seq:::::::

TAANACCGTGTAAATTGGGATGGGCAAAAGGCCAAGCACCAGCGTGGCCACGAACGCCGGAGGGACAATCTCGGGC  
GGCTAGGGCTCTCGCGGGAAAGGCCGACGTCAGGGTTCAACACGTCGCGTCNCCTCCGACCGCGAACATTGCG  
GGATGGCAGCAACCTGGTAGCNCCCTGGCGGGCGATGATCTGAGCGTCGCCGCGGGTAGTCGCCGCCGGCG  
ACAGTCTGAAACCGGATGACCATCGATGTTGGATGAGCAGTCAGCAACGGTTCTACACGGGATATGTTCGCC  
TCGCTGCCCGGTGGACCGGTTGGCTATCCCGAGACCGACNTCCGATCGAAGCGACCGTCTCCTGATGGACGCC  
GGCGCGTACCCCTGGGTTGCTACCGCCTGGCGTGGCCCAA

Clone Rv179

:::::::Rv179SP6.seq:::::::  
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GAATGCCCTCCGAAATCGCAGGCCGACTCCAGTTGGCGAGCAGTCAGCGTGCAGCTGCCGCCCTGCCCG  
CACGGCACCCACATGCGGCAGTTGTCCACCTGGGCCAGCGCCCCGCCGCGAACATGACCGTCTCCTGATGGACGCC  
GCCCGCATCGTGGTAGCAGCCAACGCCATGATCAGCGTCCGCGAGCGCGGGTAGCTTGCCTGCGGTCACCTAC  
GACCGCGACATTGCCCTGCCGCCCCGGACAAGTCGATCGTCAAGCGGCCACCCN

:::::::Rv179T7.seq:::::::  
 CGTGGCACGAAACGCCGGGAGGGACANTCTCGGGCGGCTAGGGCTTCTCGGGGAAGGCCGAACGTACGGCTTCA  
 ACACGTCGCGTCGCCCTCCGACCGCGAACATTGGCAGAACCTGGCAGCTACCTGGCGATGATCTG  
 CAGCGTCGCCGGTAGTCGCCGCCGGCGTACAGTCTGAAACCGATGACCATCGATGTGTGGATGCATCATC  
 CGACGCAACGGTCTACACGGCGATATGTTNCCTCGCTCGGCCGGTGGACCGGTGGGTCTATCCC

Clone Rv17

:::::::Rv17SP6.seq:::::::  
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 CGAATTTCGCCGCCGTGACCATCCAGCCCACGGCAGTGGCAGCCGGGGCCCCCGGTGCGGCATAACTGTTGGCGT  
 CGCCGTACATAAAGCTCGAACAGCACCGAACCGACTCACCACCGGCCGTGCGCCTCAAATCCACGCCGATCTCCA  
 CATACCGGGAAAAGCTCGGTGCCCCATCGGTTTCGGCTTGCCCCCAGCTGCACACCACCGGTGGCCTCGGCCACCT  
 TCGCGCCTGAGCGCAGCTACNCATCCTGACGATCATCACCCCCCCCCGGCTCACGCTGGCCTCCGTGACCGCACG  
 CATCGCCCGGTTGCGCGCACCGCGACGCCGTACAGCCGCGCAC

:::::::Rv17T7.seq:::::::  
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 CGAACCCGATGTGGGCTCCGATCCGGCGCGATGGCATCGACGGCAGCGCGATCGATGACGGCAGGCTTACGAGC  
 TTGAGGGTGTGAAGTTGTGGACCACCAACGGTGTGGTAGCGGACCTGCTAGTGGTATGGCGGGTACCGCGCACTG  
 AAGGGCACCGAGGGGAATCAGCGCTTGTGCGAGGCTGATTGCCCCGGATCACCGTGGAGCGCGCAACAAAGT  
 TCATGGGACTGCGTGGCATCNAACAGGGCGTACCCGGCTCATCGCGTCNGGTGCCAAAGACAACTTGATCGGCA

Clone Rv180

:::::::Rv180SP6.seq:::::::  
 CTCAAGCTTGGCGATGCGGGCTGGCAAAACTGGCCGGCGGGGTTGGCTTGTCAATCAAGGGTGGTTGCCG

:::::::Rv180T7.seq:::::::  
 CCGAAGGCCGTTCCCGGGCGTTAGCAAGCGATCGTCGGTTGGCCACTGCGGTGAATCTGCGGCCGCGCGGT  
 CGTGGAACGCCAGGTACCCGGCGCGTAC

Clone Rv181

:::::::Rv181SP6.seq:::::::  
 ATACTCAAGCTTTCTGCTCATGAAGGTTAGATGCCGTGCTGCTTAAGTAATTCTCTTATCTGAAAGGCTTTT  
 GAAGTGATCACCTGACCGGGCAAATAGTCACCGGGGTGAGAAAAAGAGCAACAAGTGAATTAGGCAATTGCGG  
 TGTTGATACAGCGGTAATAATCTTACGTGAAATATTTCGCATCAGCCAGCGCAGAAATATTCCAGCAAATTCA  
 TCTGCAATCGGCTTGCAACCGCTGACCACGTTACAAGCACTTGTGGCGATAATGTTACCCAACTGGATAATG  
 CAGCCATCTGCTCATCCAGCTGCCAACAGAACACGATAATCACTTCGCGTAAGTGCAGCAGCTTACGACGGC  
 GACTCCCATCGGCAATTCTATGACACCAGATACTCTCGACCGAACGCCGGTGTCTGTTGACCA

Clone Rv182

:::::::Rv182SP6.seq:::::::  
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 GACTACGTTGCCCTCAATCAGCTAACAGTCACCCCGTGGCGTGTGCGCAGCATGAAGGTGGCGCCCGACGATG  
 TGGCGAAGGCAACAGGTAAAACCTGGTGGCATGGTCGAGCCCTCATTGGCGTGTGGGATCGGGTTGCACCGC  
 GCCGGAGTGGCGGTGCAACTAACACCGCCTCACCGATCTTCGTCAGGAAACGCCGGTGTCTGGGTATAC

:::::::Rv182T7.seq:::::::  
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 TGCACCGACCCGAGCTGGAAAGCATCTCGCTGACGCTAAAAGCGCCGCGCTACCATGTCGACGACTTCGGTG  
 GCCGGATCCCGTGGACAAACGCCCATCAAGACACCCGGGGAGATCGCGATCGAACACGCCGGAAACCTGGGCC

:::::::Rv183SP6.seq:::::::  
 CGACTCGACAAGCATTCTGACAGTTGGCTCGGCATGGTAGCCAAGGTTCTGGCTCCCACAGATCATCTT  
 GGTCCGGTAGCGCTCGTCCGGTATGCTGCCGCCGGATTCTCGCTGCTATTACTCCCCCGAAAACGCCACCGGTC  
 CAGCGCGTGGCCGCCGGTCCCCATCACAAACTGAACCCCCAACAGGGGACATGCTTAGCGGTAGGGCGCGGCCA  
 AGGCAGCAATCGCATCTGCGCTGCCGTCACTATTACCCACCCGACTTCACTCCACGACCCGAATGGCG  
 CCCGGTATTGATCATCTGCGCACCGCGATAATCGGGATTGCCAGCCATTGACTACCGCATGCGAGTCATCGG  
 CTGACCGCAGCGGTCCGATTACCGAGCGCCCGANTACATCTCCTCAATATCAATGGCGCAA

## Clone Rv183

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GCGGTNTAGCTTCCCGTACCGGCACCGCCAGCCGAGAAGCTCGTTCCAGTGTGCTGGGATTCTCACGCT
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GGTGTCTCCATGGACTTGGGATGTGCCTGAACCGGTTCACCTACGACTCCAAGCTGGCCGCTCTCGTCCGAGGT
CGTTGCTTGCATAGCCGGAGGCCCGGATCCGCAATGACGGATCCATGCCAACGCTCCGAGTTGCATGCGGATCGA
CTACGAATTGATCACCCAGAACCATGGCGTATTACTGCCTGAAGTACCTGGTGCAGGATCTGCTATCCGGC
GGTGACGACCCCCGGCAAGCCGCATCCGTGCTGTGT
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## Clone Rv184

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CTCAAGCTTGGCGTGACGGCACCGGGGCACTCCGACAATCTGTACCCACCAAGATCTACACCATCGAATACGA
CGGCGTCGCCACTTCCGCGTACCGCTCAACTTGTGTCGACCCCTCAACGCCATTGCCGGCACCTACTACGTGCA
CTCCAACTAACCTCATCCTGACGCCGAAACAAATTGACGCAGCGGGTCCGCTGACCAATACGGTCGGTCCCACGATGAC
CCAGTACTACATCATTGACCGAGAACCTGCCGCTGCTAAAGCCACTGCGATCGGTGCCGATCGTGGGAACCCACT
GGCGAACCTGGTTCAACCAAACCTGAAGGTGATTGTTAACCTGGCTACGGCGACCCGGCTATGGTTATTCC
```

## :::::::::::::Rv184T7.seq::::::::::::

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CGGGTGTCAATTGGCACCGGGCGGCTGTCGGGAAATGGCGGCTCCCCGGTGGTTTGCTGAGGGAGTGCTGAACCG
TAGTCGAAGTGGGGCGCGTCAAGACTCCACCCAGCCAGCAGCGCGAAGCTGAATCTCCAACCGGGTTGTCGATC
CGGACAGGGTGGGGTGCCTTGGGCAATGACAGGTGGCGCGGTGCGTCCGGTCCGGCGGAGGTGCTGCGTTG
GGATCGCCCGGCTGGGATTCCGGTGTGGCGCGCCGGTGGTGGGGGGCAACANGTGTGCCGGTGCAGGGTGG
GCTGCA
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## Clone Rv185

```
:::::::::::::Rv185SP6.seq::::::::::::
NCTTGATATTGGCGTCAACGGTGTGGCACCGCGCTCTGCAGTTGGTAGGCCCTGCAGTTGTGCATCAGGCCATGC
CGCGCCCTCGTGGCACGATGTACAGCACACGCCGCCCCCTCACGGCGACCATGCCAGCGCGTCCAGCT
GAGGCCCGCAATCGCAGCGCGTACCCAAACACATGCCGGTCAAGCACTCCGAATGCCACCGGACAGCACGTG
CACCGTCCGGTGGGCCGGGATCTGCCCGGACCAGCGCACATGTTCCACGTCTCGTAGATGCTGGTGTAGC
CGATGGCGCAAACCTCCCATTGACGAGTCGAATCCGCCTCGCGACCCGCTCAATGTGCTCTCGTGTGCGCC
GCCATTGCGATCAAGTCAGCAATGGTATCAGGCCAGACCGTGCTCNGCG
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## :::::::::::::Rv185T7.seq::::::::::::

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CATAAGGGCGCGTACCGGTACCGGCCGCGGCCCTACACGTGCCGGAACTGGAAGCGCAGTAAGCCCTCAACCGC
CCACCGCTTGGCCCGCGCCGGCGTAGGCGCATGGCGGTGGCGTGGGGCGCGCACTGCGACCTCACCGCG
CTTCGAGCTTGTGATCAACCGGCAGCATGGTCGAGGATGCATTGAGACCATATTGAAATTGGTTATCGG
GGGCCCGATCCGATGCCCTCCAGTTGCGTGAGCAAGCAGCGGAGTCGTCGCGGGATCGATGGCACGGGTGTT
CAATGGCGATGGTCCGCTGCCCGACTGGCTCTGCGGGAGAGCCGATAGCACCAACCGATCCGCGACGTGGA
CCGAAACCGCCGAGTAGATGTCGAAAGCGT
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## Clone Rv186

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:::::::::::::Rv186SP6.seq::::::::::::
CGTCCTTTCCCAAGATAGAAAGCAGGAGAGTGTCTCTGCATGAATATGAAGATCTGGTACCCATCCGTGATACA
TTGAGGCTGTTCCCTGGGGTCTGTTACCTTCCACAGCAAAACACGTAGCCCTTCAGAGCCNNATCTGAGCAANAT
GAACAGAAACTGAGGTTTGAAACGCCACCTTATGGCAGCAACCCGATCACCGGTGGAAATACGTCTTCAGCAC
GTCGCAATCGCGTACAAACACATCACGCATATGATTAATTGTTCAATTGATAACCAACACGTGCTCAACCCGTC
CTCGAATTCCATATCCGGGTGCG
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## Clone Rv187

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:::::::::::::Rv187SP6.seq::::::::::::
CTCAAGCTTCATGTCCGTACGGCTCGGTACGCTCCGTCGAGTGTGCGAGTGATAAAATGACGACCGGGACCTCGTC
GGCATCTCCATAGCCGCCACACCTTCAGTTGCTACCGGAATCCAACCGGTAGAAGGTGGCGAGCGCTCGCATT
GGTCATCGGGATATGCCGCTCGGACGGTCAGAGCCCTCGGTCCGGCAGCACTCCGAGGCTTGTGCTGGGTGGTC
GCGACACGCATGGGCCACCATCGCATTCAC
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:::::::Rv187T7.seq:::::::  
 NCGCCGCCAGCCACCACGCCGGTCGGCGCCGGGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACC  
 GCGACACCACCCGGCTCGCCTACGTCGAGCCATACCGGGCGGAGCTACATCGCTCGGCCAGTGTTCGGCCCT  
 CTTTCGAGGTGAGGTGATACCGATTGCGCATCCGCAGCCGACCCCTGGACGACAGAACCGTGCCTACGANTGCT  
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 TTCCGGTGTGAT

Clone Rv188

:::::::Rv188SP6.seq:::::::  
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 CACGCATATGATTAATTGTTCAATTGATAACCAACACGTTGCTCAACCCGTCCTCGAATTCCATATCGGGTGC  
 GTAGTCGCCCTGCTTCTCGGCATCTGATAGCCTGAGAAGAACCCAACTAAATCCGCTGCTTCNCCTATTCTCC  
 AGCGCCGGG

Clone Rv189

:::::::Rv18SP6.seq:::::::  
 ATACTCAAGCTTCAACCGATTGACGCATTGCGAAGTGCACGGCGCCCGCATGGCAATCCGGAAGACCATCATTG  
 GCCAGTGGCCGGCGCTAACAGGTTCCAGCCCCCCCACCGATGCGCTCGAACATGCGGTGCAACCCATTGCGAGGCCG  
 GCAGGGAAAGCACCGCGGAAGCCGAAAGGGCTGCAGTTCCGCGCCAATAGTGTGTCGCCAACCAGATGCGCTCGA  
 AAACCGCGCCGGCAGTCAGCGCACCCGACCGAGGTCGAGAGACGTCGTAGCGCGCCACATGGGGTGCCTACGGC  
 ACGGCAGGTAGGCCGCGCAACCGAACCGTGGTGATGCCACGGTCCGCAGGAGGCAGCACCCGCAATGCC  
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Clone Rv18

:::::::Rv18T7.seq:::::::  
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 CCGCGAGGCCATCGACCGATTACTGCCACCGGGTGCAGGAGGGTGCAGTCCGCTCCGTCAGCTCTCCGACGA  
 TCCATCCGGCTTCGCCGCGGGTGGCGTAGCCGTCATGAAATCGCTGCCGGCGTACCAAGGTGATTCTGTC  
 CCGTTGTGTCGAAGTGCCTTCGCGATCGACTTCCGTTGACCTACCGGCTGGGCGTCCGACAAACACCCGGTGAG  
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Clone Rv190

:::::::Rv190SP6.seq:::::::  
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 CAGCTGGGATCGCAGCTTCTATGGTTGCGGACGGGTGCGAAATCACGGTGGCGGTAGCCGTTGCGCTGATTGGA  
 CCGCTATCGCTGCCGTTGCGGTAGCCGCCCCGACAGGGCGTCCGCTCAGCCCCATCAAGGCGCGATAACGT  
 CGAGAGCAGCCCGCGCAGCAGATCCGGCTCGCTGTGCGAGTTGGTCAAGCAGAACCTGCTCGGTGT

:::::::Rv190T7.seq:::::::

CCTTAAGCCCCGAGGGCCCGCACGCCGGTACGCCAACAGATCGTCATGTTGCGTCGTCCGCC  
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 CGGGCGACTGCAATGTCATGACACCGACGGCGCCGATGGGCCAGGGTCTGGCAGATTGATCTGTGCGCCAGTG  
 CCAGCAGCGTCGCTCGTCATACGCCGGCGACGAGTTGAAACCGACATGGCAGGCGTCGCCGTCAGTCCACG  
 GCACCAACGCCGCGGGCTGGCGGTGAGATTCCAGACTTGAAAGTACGGAACCCGCTGCCACCACAGCAGAACGTG  
 AAACAGCAGCCCGCGTGGTAGGCCGATGCCGAGGGCCGGTGCAGCTGGCAGTGGCAGGAGATCGTCAC  
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Clone Rv191

:::::::Rv191SP6.seq:::::::  
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 ACGGCAGCGGGTGGGTGGTCAAGTCCGGTCTACGCTTGGGCCAGGACGCTGGCAGCTGGCGGTGCG  
 CGCAGAACGCGGGCGGTCGGGTGCCATCAGGAATGCCACCGCCGGCAGTGCACGCCAGTGGCGGCGATGTCA  
 GCCATCGGGACATCATGCTGCCGTTCAACTCCTCGACCGAGTCGGCGGAACAGCTCGATTCCGGACCGCCAGCGCA

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TTGCCGCT

:::::::Rv191T7.seq:::::::  
CGGTCCGACCCCTGTTGACGGTACCTGAATCAACCCGATGCCACCGCCGCGCGTTCACGCCGACAGCTGGTACCG  
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Clone Rv192

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:::::::Rv192T7.seq:::::::  
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Clone Rv193

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:::::::Rv193T7.seq:::::::  
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Clone Rv194

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Clone Rv195

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:::::::Rv195T7.seq:::::::  
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Clone Rv196

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Clone Rv19

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Clone Rv1

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## Clone Rv201

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## Clone Rv204

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## Clone Rv205

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## Clone Rv207

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## Clone Rv209

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## Clone Rv20

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GCGGATGTGGATTCAAGCGGCCACCACGATGAGTATCTATGAGGGCACCTCCGATGCCGCTGGCGTCNGCACCGCA  
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## Clone Rv214

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## Clone Rv215

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## Clone Rv217

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## Clone Rv218

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## Clone Rv219

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GGTAGTGNCCGCCCGGGCGGCTAC
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## :::::::::::::Rv219T7.seq::::::::::::

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TTCGGGTTCAAAGA
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## Clone Rv21

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## :::::::::::::Rv21T7.seq::::::::::::

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## Clone Rv220

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## :::::::::::::Rv220T7.seq::::::::::::

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GCAGCTTGGCGGGCGCGCTTCAGCGTAAAGTGAAGCTACGGTCTTACGATCTCCACCGGGATGA
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## Clone Rv221

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CAGTCCATCGAACCGTCGACCTGATGGCNCCGGCCGGAAAGCCGCCAGTCCACCGTCTCGAACCGGGTGGAT  
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:::::::Rv221T7.seq:::::::  
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Clone Rv222

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CCCACGCCGAGCGGGCAACCTCAGCGACTCGATTACCCGGACGAAGTCACTCTACAGGTGGCCAGAGAGCTTT  
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:::::::Rv222T7.seq:::::::  
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Clone Rv223

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:::::::Rv223SP6.seq:::::::  
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GGCGTCAACGCCGAGGGCTACCGAGAGATCCTGGCATCCAGGTACCTCCGGAGGACGGGGCGCTGGCTGGCG  
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GCGATCGCGCCACCCCTGCCGAGCGGCCGAGCGCTGCAGAACCCACTACGAGCCA  
CCGAAGCCCTCTGGCGTGGGTGCGACCCCTGCTGCACCTACGACCAGGCC  
AATATGATCGGGTCTCGAC

Clone Rv224

:::::::Rv224SP6.seq:::::::  
ATACTCAAGCTTGTCAAGTTCATGGGCCAGCAGAACCAAGAGCATCGGGACATACGGAGTCAACTACCCGCC  
ACGGTGATTTCTTGGCGCCGCTGACGGCGAACGACGCCAGCGACCAATTCA  
CAGCAAATGCCAGCGCGTGCCGG

CCACGAGGTTGGTGCTCGGCGGCTACTCCAGGGTGC GGCGT GATCAAGATCTCACCGCCGCACCACTGCCCGGC  
TCGGGTTCACGCATCCGTTGGCGCCGCC

:::::::::::::Rv224T7.seq:::::::::::  
GCCCGTGTAA T TGGGATGGGAAAAAGCGAAGCACC CGTGGCCACGAACGCCGGAGGGACAATCTCGGGCGCT  
AGGGCTTCTCGCGGAAGGCCGAACGTACGGCGTTCAACACGTCGCGTCCGCCCTCCGACCGCGAACATT CGGGAT  
GGCAGCAACCTGGTAGCACCTGGCGGCGATGATCTGCAGCGTCGCC 3CGGGTAGTCTCGCCCCGGCGC

Clone Rv225

:::::::::::::Rv225SP6.seq:::::::::::  
ATACTCAAGCTTCTT GACCGAACCGCGTCCACCGCACC GTGAGATTGGTGGCGCATT CGTGTGGTAGCTGCTG  
TTGGCGCGT CGCGT ATT GTGCGGGCCAGCCTTGTGCGGGGGCGCTTCAACCCACA GTCGGCACTTCCGCAACCG  
CCCAGCTGACCGCGAATTACGGCGGCCAACGGCCGCCGGAAAGGC GTCACGCAATCGCTTATCCTTCCAGGTTCC  
CAAATCCTCCGTTACTTGGGTCTTCATCGG

:::::::::::::Rv225T7.seq:::::::::::  
GGCAGCGGCACAA CCGGAACGTCCGACGGTGTCAATCACGGGTGCACGGTGTGCATCAGAA TGGCGGGGTTCGT  
TGTCGCGGTGAGGC GTT CGCGAGGAGGTAGTGTCTACCCCTTGCCCGGGTTGTGCGGACTGAAAGGATTTCAT  
TGGGAACCCACGGCTCGTATCGCAGGGCTCGGTGACGTCTGTTCTCNAGCTCAGGAAGTTCGGCGAGAA TCTCG  
GTGGATGTTATTGGTCCCGCTAC

Clone Rv226

:::::::::::::Rv226SP6.seq:::::::::::  
ATACTCAAGCTTCTCGGCTCTCTGATAGCCTGAGAAAGAAACCCCAAGTTAATCCGCTGCTTCACCTATTCTCCAGC  
GCCGGTTATTTCTCGTCTCCGGCTGTCA TATTAAACTGTGCAATGGCGATAGCCTCGTCA TTTCATGACCAG  
CGTTTATGCACTGGTTAAGTGTTCATGAGTTCA TTCTGAACATCCTTATTCA TTGTTGCGTT

Clone Rv227

:::::::::::::Rv227SP6.seq:::::::::::  
ATACTCAAGCTTGGTGACCGGCACCGCATA CGTGC GG CAGGCATCTGGCTGGCGGTGGTCCCGCTCCGAAGCC  
GTCGAACACC ATCGCCAGCGCGCTCCACATCAACGACCATT CGGCCAGCTT GCGCGCATCAGCGGTTGTCGAT  
GAGCGCCCACCGAATGCCGCCGCTGCCCGCGTATCACATCGATT CGACC ATCGCGCGCGCGCGTTGCCGAGGGC  
GAACGAGCGGTGCCAACCGCAATCTGTTGGTCAGCTCCCTCATGCGGGTTGATTCTT GCGTCCGGACGGGCC  
GCGTCATGCGCTCGGTTCGCC

:::::::::::::Rv227T7.seq:::::::::::  
CCGTTGCGCAGCGTGAGCCGATAGT GACATCCGGCTCGGTGAAGGTGAAATCGATGCCAGGTGAGGTCCCATGCG  
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ACTTGGCCGGAGCTGCCGGGTTCCCGTGCAGCTGGCGCCGGTCA GAAAGAAATTGCGCCAGGTGCGCACAC  
TCCGCGCCGTAGGCCAGCTGCTCCAGGGTGTGCGCATAGAGCCCGGGCCGCGACGCGTGTGCTGCGTGGCGAACACC  
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Clone Rv228

:::::::::::::Rv228SP6.seq:::::::::::  
ATACTCAAGCTTGGGATGTTACCCCTGACAGCGTGA ACTATGTCNAACACACGGCACCGAACGGTGTGTTGGGGAC  
CCCATCGAGTTCGAGTCGCTGGCGGCCACTTATGGCTGGG TAAAGGCCAGGGCAGAGGCCGTGCGCATTGGGTG  
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GGGCACATTCCCCCACTTGCACCTCACCGGTGGAACCCGCCATCAACACGTCGCGACGCGGCTGTTGCG  
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:::::::::::::Rv228T7.seq:::::::::::  
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CGGTCTCTCGAGTATCTCCCGCACCGCCCCACCGGTGCGGTCTGCCCGGATCCACTT GCGCTGGCAGCGAAC  
AGTCGTCGTAACGGGGCGGTGAATGACAGCGATCTCGACCCGCCCTCCGAATCGGCACTGCCGGTGC  
CCGCACCGGGCGCGTACACAATCCGGCCGCCGAGCGCCGGGGCGACGANTTCTGGATCGACACCTCAACTCCTG  
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## Clone Rv229

:::::::Rv229SP6.seq:::::::  
 ATACTCAAGCTTGTATGCCGCCGAAACCGAGCGTGAGCACGCCACCCACCACGCCGGGTGGGCGCCGGGGCCCG  
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 GAGCTACATCGGCTCGGCCAGTGTTCGGGCCCTTTGAGGTCGAGGTCTATACCGATTGCGCATCCGCAGC  
 CGCACCCCTGGTCGTCTCGTACCGTGCCCTACCTCTGCTTGTGCGGGGGCCA

:::::::Rv229T7.seq:::::::  
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 GCCCACACCTCAGTTGCTCACCGGAATCCAACCGTAGAAGGTCGGCGAGCGCTGGCATTGGTCATCGGGATA  
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## Clone Rv22

:::::::Rv22SP6.seq:::::::  
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 GGCTCATCTTGATGATCA

:::::::Rv22T7.seq:::::::  
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 GCTTCCCGGATTCAAATCCGGCGCGTGTACCTGGCAGGGTGCCTTACCCACCGGACCATGCGCATAGAGGATG  
 ACCGGCCACGATCACGGTCCCGGTGATCGGGCCGCTGCGGGCCAAGGAGAACACCCGCCGGTGCACGCCACCTCG  
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## Clone Rv230

:::::::Rv230SP6.seq:::::::  
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 GGTCGACTTGATCAAGTCGGTGGATACCGGGTCCGGCCGGTGAATTGAAACGGTGTGCTCGGGCATCCGGACGT  
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 TGTCGATGCGGACGGCTTATCAACTTTGTCGCCAACACTT

:::::::Rv230T7.seq:::::::  
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 GCCGCACATGTCCTCGGGCCGGCAAAACGTGAAAAACGAGCGGGCAGTGCATGACACCAGGCCCGGA  
 TGGGCCAGGGCTGGCAGATTGATCTGCGGCCAGTGCAGCGTCCCTCGTCATACGCCGGCGACGAGT  
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 TGAAAGTACTGAAGCCGCTGCACCAACCAAG

## Clone Rv231

:::::::Rv231SP6.seq:::::::  
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 CCGATCGCACAGGGTGGCCACAACCGGCCGCTTGATGCCGGTGGCAAGCCGGCAGTTGCCAACCCAGCGTGT  
 CNTGCTCNGCTCTNTANTCAGGAGAAGTGGCTCGCTGATCACCATCGGCCAGGATCTGCGTGTACACA  
 ACGCTCGCCAAGGAGGTTGTTGT

:::::::Rv231T7.seq:::::::  
 TCCGCCACGCTTGCACGCCCGCATACGGCGCGTACCGATCTCGCGTCATACACCGGGTAATGCCGACGGTG  
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 TCAACGACGTCAATCACGTTGTCGCTTCTACGGTACCGACCCGGTGGCAGCGTACTGCGCCGGTGCCTCGGCCGAGA  
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 ATTCCATTGACGGGACGCCGACCC

## Clone Rv232

:::::::Rv232SP6.seq:::::::  
 CATTCTTAACAGTTGTTGGCTCGGCATGGTAGCCAACGTTCTGGTCCACCATATCATCTGGTCCGGTAGC  
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 GGCGNCGCGGTCCCATACAAACTGAACCCCCAACAGGGACATGCTTATCGGTAGGGCGCGCCAAGGCGGAGCA  
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 TGATCATCTGGCGACCGCGGATAA

:::::::Rv232T7.seq:::::::  
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 ACATGCCGGTCAAGCACTCCGAATGCACCGGACCACGACGTGTCACCGTGGCGTGGCCGATCTCCCGC  
 GGACCATGCGCGACATGTTCACGTCCTCGTANATGCTGGTAGCCGATGGCGCGAAACTCCCCATGACGAGTCGGA  
 ATCCGCGCCTCGGCACCCGCTCAATGTGCT

## Clone Rv233

:::::::Rv233SP6.seq:::::::  
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 TCGTCTTGCAGCAGGGTGGCCGCCGACGCAAGGCCAACACCACGTCGTCGATGACGTACCA  
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:::::::Rv233T7.seq:::::::  
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## Clone Rv234

:::::::Rv234SP6.seq:::::::  
 CGCGTTGAACGAAGGGGTGCCGCCGGCTCGAGCAGGCAAGCCATTGTTGATGCCGTTACCGAAGATCTTCGG  
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 GGGAGGCGAATCATGGTCGGTGCCTGACTAGGCCCGGG

:::::::Rv234T7.seq:::::::  
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 GATTCCGTACACGCCACGCCGATCAGGCCCTGGCCAGCTGATTGGAGCTGGGTATATGCCGGGATGGTACGAT  
 GGTACGCGCTTACATTGTGGCGCCAGAACACGCCGTTGGGCCGGCGTCAAGACTAGGCCGACCANATCC  
 CGGGGTCAACAGGGTGGACCATCC

## Clone Rv235

:::::::Rv235SP6.seq:::::::  
 CGCGGACATCCGAAACGAGGACACGCGACCGCTTCGGTGTGATCTATCAGGGCTCGCACCACGCCAACCGCTTCC  
 GGCTACCTAGACGCCG

:::::::Rv235T7.seq:::::::  
 GCATGCCGGTGTACGCCGTTCTCAGTGCAGCAGGGCAGCCGACACCCACGCCGACATGCCGTGCACGCCGGN  
 GCCGGGGCGGGAAATCT

## Clone Rv237

:::::::Rv237SP6.seq:::::::  
 CTCAAGCTTCAGNCCNTCTAACGGCTCGCGCGGATGCCAAAGATGCCCTTGGCCGGGTTGGGGGTTCTGCTC  
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ANATCTTGTATGTCCTGGTGAATCCACGGTACTTTGGAGTGGAAAGGCAGGCCATACTGATCGCGCGGCCACCATGAGCTAGCGGCAGGAAAACCAGCAGCCGCTACCCCTGCGCAGCAGCGTCGGGTGATATGCCCTGGCGCC

:::::::Rv237T7.seq:::::::  
 AGTCGAANGTCAGTCGGTCTCCTCTCCGACTACGGCCAAGAACTGGGGCAGCGTGTCACTGAGAAGACAGCGGAAAC  
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 CGCGCCGCGTGCCTCAGCCGATCCACTGGATGCCCTCTCGCGGGTTCAATCAGTACAGGGCAGTCGCCACC  
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Clone Rv23

:::::::Rv23T7.seq:::::::  
 AGCTTCGCGCGTGGCGATCGCGGTTCAAGGCAGCGCTTCTCGAGCACAACAGAGCGAAGACAGCTCGGCACGGAGCCT  
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 CCGAGCGCCGTAGATGTNCGACCGGGGGTGTGATGTGCGCGCTGGTGAAGTTTACGACCTGACCATCGAAGATC  
 CGCCGATCCGAGCTGGCGGGATGCGCCGGCTAACGACATCTACGGCGGAACGGGTGAGCCCTTCACCA  
 CGCGGGGCTGTGCTACTACCGCAGCGCTTGACAGCGTCGCTGGCATGGCAGACACCATTGGTCGCGCAGCACTG  
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Clone Rv240

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 AGCTTCAGCTGATACTCGACCAGCCCCACTCGGGCCAATACGTGAATGTCAGCATCTCACCCGTTACGGGCTANT  
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 GTCGCGCCCGAGGTCAATTGTTACGGATGTATCTCGGGGCCGATCGGGCCGATGTGGCGCCGCGCCGCTGG  
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 CGCGGCCGCGGGTTGCGATGGCNCGCGCGT

:::::::Rv240T7.seq:::::::  
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 GAGCTACATTGACCAACTAACCAACCGGTTGGGTAGCGGTGATCTGGCGTGTGGTCTTCACCTGCG  
 TGATAGCGATCAAATGAAGAATATGCGGAGTCTAGGGCGGAGCGCCTGGCANCAGTAGATCATCGGCTCACGGGATG  
 CGGCCTCTGGTACGGACATGCGCGCG

Clone Rv241

:::::::Rv241SP6.seq:::::::  
 CTCGTGAGTAGCACCCCTGTAATTGGGATCGGAAAAAGGCGAATCACCGCGTGGCACGACGCCGGAGGGACN  
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 AACATTGGGATGGCAGCAACCTGG

:::::::Rv241T7.seq:::::::  
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 AGCGCGTGCAGGGCACGATGTTGGTGTGCGCGCTACTCCATGGTGGCGCGTGTGACATCGTCACCGCC  
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Clone Rv243

:::::::Rv243SP6.seq:::::::  
 AGGACCGTCAGCACGGCAGCTGCTACTCGCCGAGCAGTGGGAATCGCTCTGCAGCAAACCATTA  
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 CGACACCGGGGCACTCTATGACCCGACGGACGGCTCGCGGTACTGCTGGTTCACCGCGACGCCGCACGGTACG  
 CGTCGGGACTGCGCTGAGTCCANCTCGACGCCGTAGCGCTGCTGTGCGGCCATGTCGGCATCTACCGCC  
 CTCCCTTGAA

:::::::Rv243T7.seq:::::::  
 CGACTCTGTTGGCACTGCGGGTCGATCTTGCAGGCCGCCCCGGTGTGGAACGCCAGGTCA  
 GGTCAGCGCGTGTGGCCAGCGTGTGGTACATGGAAGTGGTGTGACGAGCGACTTGGCGTTGGCAGCAGCC  
 GCGGATCGCCGAGGGTGTGAGTCCANCTCGACGCCGTAGCGCTGCTGTGCGGCCATGTCGGCATCTACCGCC  
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 ACCNGTATCCCACGGTCAACCC

## Clone Rv244

:::::::Rv244SP6.seq:::::::  
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 CGCGCCCGCAAATGCTGGTGGCGGGCGGTGGTGGCGCTCGCATGGCTGGGTGGCTGACCCAACCTCTCGAACCA  
 CACCGTGGGTGGGCTGGCTATGGCCTGCCATATCGGCTGGTGTACN

:::::::Rv244T7.seq:::::::  
 CCGATATCCGAGCCGATAGCTGGCGGGCTCGGGTGGTNGCCAGCGGCCGTGCGACGAAAGTGTGACCGTCATGAAACA  
 GACACCACCGCGGCCGTCGGCGTGTACCTGCTGAGATCTAGCATCCGACGCCGTGTGATCGCCTTCGGC  
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## Clone Rv245

:::::::Rv245SP6.seq:::::::  
 GCTTCAGGACAAATTGNATCCTATGCACCGTGTACGCCATGAGTGAAGACTGCACGCAATGCCCGAATCCGG  
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 GCAGAAGGCGCCTCGTCCGGTCCATCTACGCCAGACACTGGTGTAGCAGGATCGGCACTGGTCAACATCGGTGCCGACGGTGG  
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 TCTCCAAC

:::::::Rv245T7.seq:::::::  
 GTTTGGCGGCTTATTGCACTGAGGTGTCATTGACCCACAGCGGAAATGCCGACTATTGCAAGGCCTCCTCGCCT  
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 TCGAGGATGAACCTGGCGTTGAAATTGTCAGCCGGCCATTACATCGAGGCCAGATTGTCACACATGGCGGGCG  
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## Clone Rv246

:::::::Rv246SP6.seq:::::::  
 GCGCACTCCTCTTATCGCTCCGCTCGCATCGTCGCCGCCGGTCAGGTGCAAACGCCCTCGGGGTGGGGTCCCTG  
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 CAGCTTATCAGTGTGCAACGTGCGAACGTCGCGCTCGCCGGTGCCTGAATCTCTACAAG

:::::::Rv246T7.seq:::::::  
 CGCTGAAAGGCCACCATTGCGGGTCGGGCCGGCTCGGGCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCG  
 CGACACCACCCGGCTGCGCTACGTCAGGCCATTACCGCCGGAGCTACATCGCTCGGCCCTAGTGTTCGGGNCC  
 TTTCGAGGTCGAGGTCGA

## Clone Rv247

:::::::Rv247SP6.seq:::::::  
 TGTAATTGGGATGGGCAAAAGCAAANACCGCGTGGCCACAAACGCCGGGAGGGACAATCTGGCGGCTAGGGCT  
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:::::::Rv247T7.seq:::::::  
 CTTGGGCAACATGCTGAGGATCGCCTTTCAACCACGCCGTGGTGGCGTTGCATTAGCTACCGATGGTGCCTTG  
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 GTTGATCACGATGACGAAGTCACGCCATGACATTGGGGCGAACCTGGCTTGTGCTTG

## Clone Rv249

:::::::Rv249SP6.seq:::::::  
 GCATGCTTCATTATCTAATCTCCAGCCGTGGTTAACAGACGATCGAAAATTGATGCAGACGGTCCAAATAGAAAG  
 ACATTCTCCAGGCACCGAGTTGAAGAGGTTGATCAATGGTCTGTTCAAAAACAAGTTCTCATCCGGATTGAACTTTAC  
 AACCTCATCCGTTCATGTACAACATTTTGAANCATGCTTC

## Clone Rv24

:::::::Rv24SP6.seq:::::::  
 ATACTCAAGCTTGTATGCCGCCGAAACCGAGCGTGAGCACGCCAGCCACGCCGCCAGCGCGGGTGGCGCCGGGGCG  
 GCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCGCGACACCACCCGGCTGCCATCGTCTATCCATACCGGGCG  
 GAGCTACATCGGCTCGGCCGCCATTGTCNGGCCCTTTCGAGGTCGAGGTCTATACCGATTGCGCATCCG

:::::::::::::Rv24T7.seq:::::::::::::  
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Clone Rv251

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TGTTTGATGGACCGGGGTGATTTGATCACGAAATGGGTGTTATNCAGGTCGCACGCTTCATCCGGGCGGAA  
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:::::::Rv251T7.seq:::::::

GGGTGTGCCGTGCTGTATGCACGGCATACGGACATCCTCCCCCTGAAGACCCGCGGTCAAACAGCCACGTGTCCATC  
ATCANGGGTCAACCCCGGCAAGGGCGACGGCACGCCAAGTTCGCCGACCCTAACCTAGTGTCTAGCTTCATTT  
GCTCGAGCAAACAGCTGGTCGGNCCTAGGAATGAACTCAACCGATTGGTGCCGCGTAGGTGTCCCTGG  
CTG

Clone Rv252

:::::::Rv252T7.seq:::::::

ACTACCCGGCCAACGGTGATNTCTGGCCGCCGCTGACNGCGAACGACGCCAGCGACCCACATTAGCAGATGGCCA  
GCGCGTGGCGGGGCCACGANGTTGGTGCTCGCGGCTACTCCCANGGTGC GGNCGTGATCGACATCNTACCGCCGCAC  
CACTGCCCGGCCTCGGTTTACCAAGCCGTTGCCGCCGCAGCGGACGATCACATCGTTTATTTNNNTTNCNGGAAT  
CCCTCGGGCCGGCGCTGGCGGGCTGATGA

Clone Rv253

:::::::::::::Rv253SP6.seq:::::::::::::  
ACGTCGGGANACTGTCGCGTTCATCCTCGTCTCGGCGGATTGGTCTGCTGCGCCGGACCGACCGATCTCAGCGGGGGTACCGCTCCGTGGGGTGCCTA  
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:::::::Rv253T7.seq:::::::

GCTCAAAGGCACTACTGGCACCAAGGCCACACGTACCTGTGACTCCTGCGCCGACCCGCCGAGGTCTGGCCGTTA  
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ATGACGGGTC

Clone Rv254

:::::::::::::Rv254SP6.seq::::::::::::

CGATACCGGCTGTTACCGAGACATCCACCATGCCACCGAATCACCGCACGCCGAATCGCACACAGCTTGACG  
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CACTTGCCCAGCAGGGGTTCGATGAGTGTACACCGAAGACCTCGATATGGCGCAATCCTGGCCGACACATCCAAC  
CGGGTGGTTGTGTGCTGGCGCCGGTGGGTGNGCAANACACTACCGCGGCCGCTGGCGTTGCGCGGGCCGAAT  
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CGTCGTCGTCGTGGTATGCGATAGCCATCCCGTGGGCTACTCGCCATACCGATCAGCTTGGCCCCGAGGCCGCCGC  
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GCTCGGTGTACANGTTGGCATCGACGACGTACGGGCCGGCTACTGCCGACGACAANGTCGCAAGCCGTGNCNGCTG  
CAAGCTGGAGGTGCCAGATTGACCGTGGTCGGTACGGTATCAACGACCTCCGGCTTAGCGGCCGCGATGTCGCAT  
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Clone Rv255

:::::::Rv255SP6.seq:::::::

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Clone Rv257

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Clone Rv258

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Clone Rv259

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Clone Rv25

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Clone Rv260

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Clone Rv261

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Clone Rv262

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Clone Rv263

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Clone Rv264

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 CATGCTGGAAGTTGTGCGCACTCTTCCCTCCGCGATGTGGGCTAACGACTCGTATTGAGCAAGAAGTACGTGACA  
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Clone Rv265

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Clone Rv266

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Clone Rv267

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Clone Rv268

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Clone Rv269

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Clone Rv26

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Clone Rv270

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Clone Rv271

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Clone Rv272

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Clone Rv273

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Clone Bv274

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Clone Rv275

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Clone Rv276

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Clone Rv277

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CGCTTGAATGTCCGGTTAACGCCGGATTCCACCATCCCTGCGAAAGGCCGGTGGGTT

:::::::::::::Rv277T7.seq:::::::::::::  
GATCGCGATCGTCGATGTGGCATCCGGCTTGGCGTGCACCCCGCGTAAGGCAGACCAAGATGGTTCGCCGACGGTCAA  
CCTGCCACACGCACTGGTAAGACTGCCCGCGTGCCTGGTAAAGGCCGATGCTGCCGTTGCCGCG  
GGGGCTGATGCTGCCGATCGACGATCTGATCGAGAGGATCAGGGCGGCTGGCTGGAATTGATGCCGAGCAGCG  
ACCGGATT

## Clone Rv278

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:::::::::::::Rv278SP6.seq::::::::::::
AGCTTACGCCGCTTCGCTTNGATTGGGACGCCCATCGAAAGCGCAGTTGGAAGCGCGGCCGGCTGGTCAG
CTGCTCAAGCAGCCGCAATCCAGCCCAGTCCCCTGAGGAGCAAGTGGTTCGATCTCCTGGGACCCGGCTCAC
CTGGACTCGGTGCCGTCAAGGATGTCGGCGTTGAAACCGAATTACTGGACCACATGCGGGC
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:::::::::::::Rv278T7.seq::::::::::::
CGACGGGACCTCGTCGCATCTCCATAGCCGCCACACCTTCAGTTGCTCACCGGAATCCAACCGGTATAAGGTCGGC
GAAGCGCTCGGCATTGGTCATCGGGATATGCCGCTCGGGACGGTCAGATGCCCTGGGTCAGCAGCACTCCTCAGG
CTTCGTCGGGGTGGTCGCGACCGCATGGGCCACATCGCATTCAACAGGTCTGCGGAATCACCAAGCAGTANACGGTT
CCTTCTAAGCAACACCGAAATTTCAGGACCCGAATGTCCTGGGAAACATGTCACGGTAAGTCCGGTATTCCGGT
ACCGGTTGAGCATTGA
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## Clone Rv279

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:::::::::::::Rv279SP6.seq::::::::::::
CGGCATCGGTTGGGCTGTCACCAGCAGTTGGTAGTTCTTCACTACTGTTGTTGAGCGTCGAGCCGCCGCGCTGTC
GAGGTCGCCGGACCGTACCCGCCAGGCCGGTCAAGGGTGCCCTCCAGTCCACGNGCTGTTGCTAACCGCTTA
TCTTCAATCGAGACNATGCCAGCTTCACTCGTGTGGCAGTCTGTCGAGGGCACCTCGAACCGGGCTGCGANTAC
AGCCACCGCAGTCGTTGGCCCTTCGCGTCGACCATCGCAGTACCGCAGGCACTTGCCTCGAGCAGCTGGCCGAT
CCGTTGGCAACGACCTCAGAGGCACGATTGGACATCAGCCCTAGCCGCGCTGCG
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:::::::::::::Rv279T7.seq::::::::::::
CCGTCGANGCCGCCACTTGGCTTGACCGACACCAACATGGCCTGAGGGTGGTCAACAAGACCGTGGCCGACGGGCTG
AACATCACCAGAGCGGCATGAGCCACGCCACCGAGTTCATCATGTTGATGCCGAAAACCATTGGGGTAGCGGAA
GAACGGTCGAGGTGCTCTACACCGAGTATTGAAAGTCAACCGCTGCTCAACGGCGTCAACATCATTTCG
ACGGGTTCTGCGAGGGAGGATGCCACGATGAACTGGATCCAGGTGCTGTTGATCGCGTCGATCATGGGTTGCTGTT
CTACCTGTTGCGGTCGCGCCGAAGCGCGGGTCCGCTGGGTCAGGTGGGCTATGTCCTGTTGCTGCTCCGGCA
TCTATGCCGTGCTGAGA
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## Clone Rv27

```
:::::::::::::Rv27SP6.seq::::::::::::
TTACACGNCTGCTTCCGGCTCGTATGTTGAGCAGGATAACAATTACACAGGAAACAGCTATGAC
CATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTTGAGCGTCGCGCAGGGCAGCTCGCCGG
CAATTCTACTAGCGAGAAGTCTGGCCGATNCGGATCTGACCAGTCGCTCGGGTCAAGCCACCCCTCATTGCCGAT
GGCGCCGACNATGGCGCCTGGACCGATCTGTCGCGCTTGCACGGNGACCGGGTANGGGTCAAGTCCGGTCTACN
CTTGGGCTTGCAGGGTCCCGACGCTGGTGCAGGGTGGGTCAGGAAACGGCGGGTGGGTCAGGATG
CCTCACCGCCGCGGCACTGNACGGCAGTGCACGGGATGTCNGCCATCGGGACATCATGCTCGCTTCATACTCCT
CGACC
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:::::::::::::Rv27T7.seq::::::::::::
CAGGCATGCAAGCTTGTACACCAAGTGTTCGACCCAGGGCCTCCATCCGGCGAGTGGATACTCCCAGCAGGTAGCA
GGTCGCCACCACGCTGGTCAGTGCCTGGCAGCAGCTGGGTCAGGTTGCGGGACGGGTGTCAGGAAATACGGTGGGAGGCTGATT
GGCAGCTTGGGATCGCAGCTGATGGGTCGGGACGGGTGGGTCAGGTTGCGGGTGGGTCAGGCTGCTGATT
GGACCGCTCATCGCTGCGTTGCGGTAGCCGCCACAGGGCGTGGCTCAGCCCCATCAAGGCAGG
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## Clone Rv280

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:::::::::::::Rv280SP6.seq::::::::::::
AGCTTAGCCAGTTTCTACTCTTGGGCCACACCCACAGTGCTCGACGGTACGGTACCCATGATGGCCATCCAGT
TGGCATCGGTGAGCTGATAATGCCAGCTGGTTGCCAACCCGGTAGCGATCTTGGCGCTGCTTGTGACTG
TACCTATCGAGCAAGACAGCCGGTTGCGACAAGATGACTTTGGATCTTCGGGACTTCGATGGGGTCTCGG
GAGTCCGGGCCACCGCAGGTAAGCCTCGTCCAGCCCCATACCTGACCGGGTATCCCAGGTGCGCAATAACG
CCACCACTCCTCGGACGCCGGTGTAGGCGGCTGGGTTGACGGCAAGAAGTGGCCTCAGGGCATCGTGGCGCG
TCCCAACGGCTGCGCGCACACCGTAGGCGGGGCTC
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:::::::::::::Rv280T7.seq::::::::::::
CCGGCGGAACCTCAGACGTGCTGGTGGCGCATGGCACCGCGGGCAGCAAAGCGCAGTCTCCGGGACGACAGCAA
GCGACCGCTAGACAAGAGGGTCTGCGCAGGCAGAAGCGTTGGTACCAAGCTGCTGGCTTGGCGCCACCGATGT
TTATGCCGCCACCGGGTGCCTGCCACCGACGATGGAGGCCACTGCCCGGAACTGAACGTGACCATACACAACGA
GCCACCCCTGACCGAAGAGTCCCTACGCCAACCCAAACCGGGCCACACCGAGTGCAGATCGTCAGCAAGT
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AGGCACACCGTGATCTGCACCGAGGGCAAGGTCACTCCGATCTGATCACGTGGTGGCGAGCGCGACCGTGTGCC  
CCCGACAGTCCCACGCAAAGGCAGCACGTTGGTGT

Clone Rv281

:::::::Rv281SP6.seq:::::::  
GTATGGTCAGCTGCCATCCGGCGCTGTCGGCGAGCTGCCAGATCTCGTCAGCGTAACCGGGTTGCGGGATCCACG  
CGTGCGGGTTGTCTAC

:::::::Rv281T7.seq:::::::  
CCGACTTTCCGCGGGTACCCGCTCAACTTGTGTCNAACCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCA  
ACTTCATCCTGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACT  
ACATCATTGACCGGAGAACCTGCGCTGCTAGAGCCACTCGGATCGGTGCCATCGTGGGGAACCCACTGGCGAAC  
TGGTTCAACCAAACCTGAAGGTGATTGTAACCTGGCTACCGGACCCGGCTATGGTTATTGACCTCGCCGCC  
TGGTGCAGTCGTTGGTGTCCAGAANGTCAGCCCG

Clone Rv282

:::::::Rv282SP6.seq:::::::  
GCACCGATGTCGGCGAGCACTCGTCACCTCCAGGGTGCCTGCCACCAAGTATTCGACGAGTATTCGTCGG  
GCCGCCGCCGGTGCAGGGTGCCTGGACTCGCGCGTACCGGCTGCC

:::::::Rv282T7.seq:::::::  
TGCACCCAACCTACTGAGCATGCTAACGCTGGTCGCGGGCTTGTGTTCCCGCGTGTGGCAGGGCACACGCTCGGG  
CGTAGCTGGAGAGGCCCGGTCAAGGCCGGAGAGCAGTGCTCAGTCCGCCAGCTGACCGACTTCGATGAGAACGC  
GCTTCTGCCGTATTGAACTGGCGTGTGACGGTCGCTGAGCAGCGCTGCCAGTGCGGCCGTGATTCTTCATCG  
AGCCAGGACGCGCATTGTTGCGGCC

Clone Rv283

:::::::Rv283SP6.seq:::::::  
AGCTTACGGCCGGTCACGCGACGAGTGGTCATGACACCACAAACCGTCAACGCCACTACAACCCGGGATGAACG  
AAATCGCTTCCCGCAGCGATTTACAGCCACCAATTTCGATCCGCAAGGCCACGAGGCGCAACTACGGCGGGAT  
CGGGCGCGTGTACGGGCACGATGATCGGGCACGGTTCGACGATAGGGGCCAAATACGANGGCACGCAATCTGG  
CNATTGGTGGATCGA

:::::::Rv283T7.seq:::::::  
ATGTCGTACGTACCAATCGCGAGGACCAATCATGCCGCCAGGGCGGCCACCCAAATGGTGGCCCGAAGCG  
CAGCTCGATCGCAGCGCGAGGTGCCGGCGCCAGTGATTACGAAACAGGGTGGAGGTGATAGGCAGGAGATA  
ACGAACGCAAGACCTATATCTGCCGTGGAGTAAGAATCGAGTAGCCGGTCGACCAACGGAAGCGAAAGTGTCC  
TGTTGATGAGCGTCGCCGGTTGTGGCGGGCGTGGC

Clone Rv284

:::::::Rv284SP6.seq:::::::  
AGCTTACCCAGCGTGCGATGCTGTCGNACACCTCCCTACTATGCGCAATTGCCGACACGGTGGCATAACACG  
GGCGATAAGGTGGACATCGCTGGGTGAACGTCGGGCTGGTGCCTCGCTGGCAATCCCGCAACCGCGTGTGATC  
GGATTCTCGTTGCCCGCAAGACAATCGGATGCAAAGCCGGCAGCAATTGCAACGCCACCAATTGCGCTGGC  
AACCTGGAAATCGAACCCCGCGGTTCGGAGCCGTTGAAACCCACGGTTCTGCGTGGCGCAGAACACTACGCC  
TACCAAATCTATGACGCGTTCGTC

:::::::Rv284T7.seq:::::::

CTGCCCGGTGGCGGTCAAGCCCTGGCAAGTCACCGCACCGCCGTCGGTTCATCGCAGGCTCCCCGAAAAGGG  
CTGGCAACAGAAGGTGATCAATGAGCTCCCGCAGACCTTCGCCATCTGGGACCGACATACGTGAAGTTCGGCCAGAT  
CATCGCGTCCAGCCGGGAGCATTGCGTGGAGTCGCTGCGGGAAATTCCGCGGCCGCTCGACCGGGTGC  
CAAAACCGACGAGGTGCAAGCTCTCGTCGAGGAACCTCGCGACGAGCCGGCCGCTGTTGCCCTCTCGAGG  
AAGAACCGTTCGCGTCTGCGTCCATGCCCAAGTGCACCTCGCGACCTCGCGCAGCGGAAGAAGTGTGGTCAAGATC  
CACGGCCGGCATCCGCCGCCGTT

Clone Rv285

:::::::Rv285SP6.seq:::::::

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GGCGCCGTCATCAACTCTCGAACATCGCGATCGGACCGGAAACCGCGAGCCGCGTCAAGCCAGCGCAACCAGC  
CGGGATCGGATGAATCATCAATATTATCAAGTGATTTCTGATGCATCGAGCTCGGTGATCTGGTCTCGGGGCCA  
GCTCGCCGTCGGCACGTCGATCCGGCGGAGCGCATAGACCGAAATAGTGCCCTCGCTTTCGCGCGCA  
AGAGTCGGATGCCGTAATATANGTTCTGGCGCGTGCCTGATCNACTCGGTGATTGATACGCCGTTCATCTC  
GGTCATGCCGTCCTC

:::::::Rv285T7.seq:::::::  
GGTGGCGCAATGACCGAAACCACCCAGCCCCGCAAACCCGGCGCCCGGCCGGCCGACAATCGTTCGTGTG  
GAGCGGGCCATCCAGACCGTTGGCGCCGTAAGGAGGCCGTGGTACGAGTCCGGCTGGTCCCGGACCGGCAAGTTC  
GACCTCAACGGCCGAGCTTGGAGGACTACTTCCAAACAAGGTGACCCAGCAGTTGATCAAGGCACCCCTGGTACC  
GTGGATCGGGTGGAAAGTTTCGACATCTTGCCCACCTGGCGGGCGGCCGTCGGGTATGGCGCGCCTGCG  
CCTGGGTATGCCCGGGCATTGATTCTGATCGCCGGATGACCGGCCGCGCTGAATAANGCCGGCTTCTTGACCGT  
GATCCACCGGCCACCGAACGCAA

Clone Rv286

:::::::Rv286SP6.seq:::::::  
CACAAATAGATTACTCAAGCTTCGAACCAGCGGCCTTACGTATCCCCGCIGAGACCTTGACCCCTAGGGCCGAAGT  
GACTTCGCTGCTGCTATGCCGACACCGATTCCAGACGCTGCTGTTACACGACGGCCGGCCGGTGGCCACCATCAC  
GCTCAACCGCCCGGAACAGCTAACACCATCGTCCCCTGCCCCATGCCGACGAGATCGAGGGCGCTATCGGGTTGGCGA  
GCGCGACCAGGACATCAAGGTATCGTGTGCGGGTGCCTCGCCGCGCTTCTCCGGCGGTTACAACCTCGCGGCCG  
GTTCCAACATTGGGGGCAT

:::::::Rv286T7.seq:::::::

TCAGGACGTTATGGTGGCAGATGGTCGCCCTGGCGCTGAATACGCGCAGCGCATGAGCTCACCGGTCGGAACAA  
CGTATCGAAGAACGTCGCACTGCTGGCAGATGGTATCTCGATGTGGTTGAATTGATCCAACTCTAAGTGTGCT  
ATCGGATCAGCGTGAATATCGAGATATTGCAATGCGATGACAGGCCATTGCGTTTATTGCTTACGCTTCCCG  
GTTGATTGCTGATGCACTGCCGAAACCGGATATGATTGTTGAAACCGTATCTACGCAATTATTGATGTGGT  
AGGCGCAGCTGCCGTTTGTGCTGCGGCTATTGATCGGGTGGGGTGTGCTGATGCCCTCTGCTCCCAT

Clone Rv287

:::::::Rv287SP6.seq:::::::  
CGCAGCTGTCGCCGATCTGGTCCGGAATACCTAGCTCAGGTTCTGAGTGGAGATGAGTGCGCCATCGAAGTGTG  
CAATGTAACCTCAGGATGTCAGGTGCCAGGCCGCTGGCGAGGATCTGGGACCGCCCATGACTTGGTCGAAGTC  
CGAACGGGGCAGCACGCTGGCGTGGTGG

:::::::Rv287T7.seq:::::::

GTAGTTCGTTATCCAAACACAGTGCCTGACCGCTCAAGCGGATCACCGACTTCACCGGGCGCATCCCACCCAGCC  
ACCGCAGTGCCTATGTCCTCGGGTGGCGGCCACCGTGGTCAACTCAACTATCCGACGCCGACTGAAGCATCGACAG  
CAATGCCGTGTCAAGATTCCCTGCCGGTCAGAGGGGTCAGCAGGGGCCGGAAAAGATACCAGGGCGCCGTC  
GGACCGA

Clone Rv288

:::::::Rv288SP6.seq:::::::  
TCCGCTCGTTCTCCGAGAGGGTTGAGTGCCAACGCTCTGCCGATGCCGAAGCCGGCCCGGTGATGACGGCGACCTT  
GCCCTCGAATGAGCTCATTTGACTACTCCCCGTGGTGTCCCTCGGATGGTGGAGGTGCCGCGAGCCTTGCCCCG  
AGGTCGGCGATCGCGTCTCGGGCTTCGGGGAGCAGACTGACCTGCAAGATGAAAGTGTGCCACATGCCCGAACCGG  
CGATGCTCGATGCTGTTTCAAGCGGCCAGGCCGTTGATCTGTCGGTCAACACNGATCGGATCGCC  
GCCGCTGCGATGACGAATGGCG

:::::::Rv288T7.seq:::::::

ATGGGAGGCCACCGATTACCATCTTGCACACACCGATTCCGGGTATTGATGTCGACGTTCCAGTCGGTCCGCAACCGCGCT  
GTGGCTGCTGCCAAAGGGGGAGGCCGATACCGAAGTCAGTCCGAAAGCTTGGGTTCCACGCTCGCGAGCCACGC  
CGTCACCTTCCACGAGACCTCACCGATCCGAAATGGAATCGGCCGTGACGGAATTGGCGCAGCGAACACTCAA  
CGAGGGTGGCTTCGTCGCCAACCGTCAACCGAGTCGCCGTCACCGTGCACGCCGACGTTCTACACCCGACCAA  
GATCCGAAAGCTGCAAGCTCCCGACCGATCCGACGTCATCACCGCTGCCGCCGGCACGTTCTGAACCTATTG  
AGCTGGAATCGGCCGTCCGGTTGCTGGGAATTGCGNTTAAGAACTGGGCCT

## Clone Rv289

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:::::::::::::Rv289SP6.seq::::::::::::
GCTTTGCGCGCTTCTCGAGAGGTTGGAGTGCCAAACGCTGCGGATGCCGAGCCGGCCCGGTGATGACGGCACC
TTGCCTTCGAATGAGCTCATTGACTACTCCCCGTGGTGTCCCTCGGATGGTGGAGGTGGCCCGCAGCCTTGCGC
CGAGGTGGCGATCGCGTCCGGGGCTTCGGGAGCAAACCTGACCTGCAGATGGAAGTGTGACATGCCACATGCCGAAACC
GGCGATGCTCGATGCTTGTGTTCTGAAGCGGCAGGGGTTGATCTGTCCGCTAACGAGATCGGATCGTCGCC
CGCGGGTCTGCATGAAGAAT
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## :::::::::::::Rv289T7.seq::::::::::::

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CTCACGCAGCCACGCCGTACCTTCCACGAAGACCTCACCTGCCGATCCGAAATGGAATCGGCCGTGACGGAAATTG
GCGCAGCGAAACACTCAACGAGGTTGGCTCGCGAACCGTCACCCGAGTCGCGGTACCCGTGCGCACGGCGAC
GTTCTACACCCGACCAACATCCGAAAGCTGCAAGCTCCAGCACCAGTCCGACGTACCCGCTGCCGCCGGCA
CGTCTTGACCTATTGAGCTGGATCGGCCGCTCCGGTGTGGAGTGCCTAGAAACTGCCCTAGAAACCGGGCG
GCACACCGCACCTGGCGGGGG
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## Clone Rv28

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:::::::::::::Rv28SP6.seq::::::::::::
TGCTTCCGGCTCGTATGTTGTGGAATTGAGCGGATAACAATTACACAGGAAACAGCTATGACCATGATTACG
CCAAGCTATTTAGGTGACACTATAGAAATACTCAAGCTTGTGACCGGGAAACCGAGCGTGAGCACGCCAGCCACC
ACNCGCGGGTCGGCGCCGGGCGGGTCGCCANGCTGCTCCGCTGGTGTGGCACGCCACCGCGACACCACCCGGC
TGCCTACGTCGAGCCATACCGGGCGGAGCTACATCGGCTCGGCCGCCAGTGTGCGGGCTCTTCGAAGTCAAG
TCGATACCGATTGCGCATCCGCGNGCGCA
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## :::::::::::::Rv28T7.seq::::::::::::

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CAGGCATGCAAGCTCACGTCGGTACGGCTCGGGTACGCTCGGTCGAGTGTGCGAGTGATAGATGACGACGGGAC
CTCGTCTGCATCTTCATAGCCGCCACACCTTCAGTTGCTCACCGGAATCCAACCGGAGGTCGGCGAGCGCTC
GGCATTGGTCATCGGGATATGCCGCTCGGACGGTCAGAACCTCGGGTCCGGCCAGCACTCCGAGGCTTCGTCGG
GTGGTCGCGACGCGCATGGCCACC
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## Clone Rv290

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:::::::::::::Rv290SP6.seq::::::::::::
GCTTGTCTATCGTCCGGCCAGGTCCGGCAGTCAGGTCGAAGGCGAGTCCGGTCTCCTCTCCGACTACGGCCAAGA
ACTGGGCAGGGTGTGAGCAGACCAGCGGAAACTGGTGGCGCCCTAGGCAGCGACCCCTCACAAACGGCGGTGA
CCCGTTCTGGTCGTGACCATCGAGCCGTGCCCAGGCCGGCGCTGCCGTAGCCGATCCACTGATGCCCTTCT
CGCGGTTCAATCAGGTACAGGCAGCTGCCACCATCGTGCAGGGCACGGTAGCGAGAAACGCCGACTTCAC
GATTGCCCTGGTGTGCCGTCGAAACAGATCGGGCCT
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## :::::::::::::Rv290T7.seq::::::::::::

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CGCGGCCATGTTGAGGTTGTCGACGGTGACGACGGTAACCACAACGTTGACCTGTCGCACACACCGTGTGGAT
CGCGAGCGGACCCGACAAATCGATGGCGGCACATCGCTTGTCCCAGGTGATTGCTAATCGGTGGGTCAAGTT
GGGCCCCAACATGACCCCGGAACCTGGCGTGGAGTACGTCGAGCGGCTCGACCCGACAATAAGCCGGCCGGCTGAC
TTGGTGAGCAGGATGGCAACACACAAGGTCGCCGATCTGTTGCCACCGATCGTGGAGAACGTCATGCCACCGGCAT
CAGGTCACTGGC
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## Clone Rv291

```
:::::::::::::Rv291SP6.seq::::::::::::
TTGCCTTCATGCCGAGCAAGGTCGACTCAGCGATGACGAATTGTTCTTCGCGGGTGTGCTGCTGGTTGCCGGC
TATGAGAGCACTGCTCATATGATTAGCACATTGTTCTGACGCTGGCCACTATCCAGATCAGCTGACACTCCTTGCG
CAGCAACCAGACCTGATCCCGCCGGCATCGAGGA
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## :::::::::::::Rv291T7.seq::::::::::::

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CGACGCTGGGCCAACTGCGACCACCAGGTCTGGTATGGCAGGACATGCCGGGTCAGCGCGCCAATACCG
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## Clone Rv292

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:::::::::::::Rv292SP6.seq::::::::::::
TAACGACTCGGGTCAGCGACCGCGAACACNAACGGCCGACNACGTGGCCAGGGTCGCCCTCCCTACAAAC
AGGATCCGTTGCCTGCGAACGACAGGCTCGGTGCGGTTGGCGCCGTGCTCCAGCGTCCGGTCCGGT
```

CCGGCGACGCTTGTTCCTCCATACTCGCCCCTAATCTCGAGGCAGGCCGTACCCGCAGGCAACCTCCAAAAATGC  
AATCCCCAAAATGCAATGCGTCNAGCTATTCTCACACCGACCGCTAGTTGCGGATCANAAATCCGTTGGCGCGGA

:::::::Rv292T7.seq:::::::

CNTGGCGGTGGTGCCTGCGAACACGACCAACTCTTGCCTTGCCTGGTATCTCGACACCGGCCGAGCCGAC  
ACCATGCGCGCGTAGATCGCGATCAGCGCTCGGCTATCGCCTGGTGCCTGGCCACCGGAATCGCCAGCCGACCGA  
ATGGGCCAGCGTTGCCATCATCAGTCCGGCGCCGACACCGAGTACGGCAACGGTCAAATCNCGTGGCGGAAAC  
GCCGGTGAACAAACGGCGGGCATCTCGCCGCCAGCGACCGCCAGGGCAGGGTGCCTGGCCAGCATCCGAGCCC  
GAGACNCAGGACCGANCCCAGTG

Clone Rv293

:::::::Rv293SP6.seq:::::::

GCTTTTNCAGCGAGCTGACCCGGTACCTCGCCGGTACCTTCGTTGATATCGCCGGCTGGTCAAGGGGGCTCCGA  
GGGAGCCGGCTGGTAACAAGTCTGGCTATATCCGCAATGCAACGCCATTGTCAGGTGGTGCCTGGTGTTCGT  
CAACAACNACTTGACTCATGTCACCGGACGGTGCATCCCANTCCGACATTGAGGTGTCGACGAAACCGAGCTGATCCT  
GGCANATCTGCAAACCCCTGGAGCGGGCACGGCCGGTGGAGAAGGAANC CGCACCACAAAGGCGCGAAGCCGGT  
CTACGACGCCGACTGCGTGCCTCAGCAGGTGCTCGACGCCGGCAANACGCTGTTGCCGCGGGGTGGATGCCG

:::::::Rv293T7.seq:::::::

GTCGTACGCCATTNGCTGGTGTGCGCATACCAGTACGACGCCGGCACCTGACGCCGGCGACAGTCGGT  
GCCATCGCCATCGCTGCCCCGGTCAACGGACGCACCTTCTCCCTGGCGACGTAGTGCCTGGCCACCCGCCCGTTG  
CGTCCCATCNATCCGGTCAACATGAGCAGCGCAACACCGAGCGGTACATGACATCGCTGTGAAACCAGTGACAGATT  
CCGCCGCCATGATGATCATGACCGTCTCCGGATTGGTGCCTGGCGAAATTCTTGGCAAACCGGATG  
CTGCGCGGCCGGCACCCGGTATCGACTCCTGCCAGGCCGGGTGTTCTGCTGGTTGGTGTGGTACCGGT

Clone Rv294

:::::::Rv294SP6.seq:::::::

GCGAGGGGTATCGCTTCCCGTCTGACCGCGACCGCCAGCCGAGAAGCTGTTTCCAGTGTGCTGGGATTCTC  
ACGCTGCTGCTGANTGCGTGCCTACCGCTTCCGCTTGGGTTACAACGAGCCGGCTACGATCGTGCACCGCTG  
AAANTGGTGTCTCCATGGACTTGGGATGTGCTGAACCGGTTACCTACNACTCCAAGCTGGCGCCGTCTCGTCCG  
CAGTCGTTGCTGCGATAGCCGGAGGCCGATCCGAAATGACGGATTCCATGCCAACGCTCCGAGTTGCATCGG  
ATCGAATACNAATTGATCACCCA

:::::::Rv294T7.seq:::::::

TGGGTCTTGCCTGGCAGGCCAGCGAAGTCGCTAGCGTGGCGTGTTCCTGGCTCGGATCTATCCTCGTTACATGAC  
CGGCACCGTGTGGACGTGACTGGCGCCGGTCAATGACACCGAGATCATGCCACGGTACGGCAATTGCTCAAGA  
AGGAAATCTTCCCNATGCAACCGGCCCTCGAACGTGGCAACAGCTACCCGCAAGAAATCGTCGATCGCTGGGTGTTA  
TTGGCTTGCCTGGTGCCTGGCTGCAAGGGTATCGACACCCACCGAGTTCAATTCTGGCGTGCCTGGCGCATTGAGCTG  
CGGGTGCCTGGCTGCCAGCACCGTCATAAGTACTTGANGATGGTCAAACGTCGGACGAACGCCACCACGTCGCTGCC  
GAACGG

Clone Rv295

:::::::Rv295SP6.seq:::::::

TAGATGCCCAAGCTGCCNTTANAGACCTCGCGACCAAGCACGGACCGACCGTCAAGGTGGGAATCCGGGTTG  
GCGTCNACCGCGTAAGGCAGACCGAGATGGTGCCTGGCAGCGTCAACCTGCCACACGGCACTGGTAAGACTGCCCGCG  
TCGCGGTATTGCGGTTGGTAAAAGGCCGATGCTGCCGGGGGGGGATGTTGCTGGGAGTGACGATCTGA  
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:::::::Rv295T7.seq:::::::

TCTCCACGGCGTGGATCAAGGTACCGGCCGGATGTTGCGCAATGGCAGGTTGTTGCCGGCTTGATGTCGCTTAG  
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AGCAACGCAATCCGTGCGGTACGGTTGGGTGCTACTCGATGTGCGCAGCCTGGCGTTGACACCATCTTGTCAATTG  
CGGCAGAGTCGATCATCCGTAAGCGCGCTTATGACCGGCCCTTGTGCCGGTNGGTAATCCGGCC

## Clone Rv296

:::::::Rv296SP6.seq:::::::  
 GCCCGGTTCGATCGGCAGTCGTCGTTACCGGAGGCCGCGTGGCCGCGTAATCGGCGTCGGCGCCGAC  
 AAGATGTGGGATATCCGCAATCGGGCGTCATCCCTCGGGCGCTCCCCCGCGTCCGAGCCTCGACGCAATC  
 GAGGCAAGTCACGACGCCGATGAGGGGCAAGCAGTGAATTACAGCGAGGTCGAGCTGTTGAGTCGCGCTCATCAACTGT  
 TCGCCGAAACAGTCGGCGACCCGGGTTGGATGCGGGCACACACCCCTACGGGGATCTGCTGTCTCGGGCTGCCGAC  
 CTGAATGTNGGTGCGGGCANCGCCGTATCNACTCCCCGTGGAACACAGCCGUGGC

:::::::Rv296T7.seq:::::::  
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 CAACCAGTANGCAACCGCCTTCAGCAGTACAACCGCCGGCGAACACTGCGAGTTGAAACCGCAGCTGCCTGGGTCAAG  
 CATGCCCTCTGCCGGTTGTCAGCGAAGGCCGCCAACAGGTAATGCGTCAACAGGCTCGTAGAAACGCCAGAACAC  
 GGCCACGAACAGCCAGTTCAGCACCGACCCGGTAGAACGGCAGATCGAAGACGAAAAACCCAATGTATAGCCGAATT  
 CGGGTCCACGATGCCAACAGGTGCCCGTGTACAACAACTGAACCTTCACCCA

## Clone Rv29

:::::::Rv29SP6.seq:::::::  
 TCCGGCTCGTATGTGTGGAATTGTGAGCGGATAACAATTACACAGGAAACAGCTATGACCATGATTACGCCAA  
 GCTATTAGGTGACACTATAGAAACTCAAGCTTACGTCGTCGGCTACGGCTCGGTACGCTCGGTGCGAGTGTGCGAGT  
 GATAGATGACGACCGGGACCTCGTCGGCATCTTCATAGCCCGCACACCTTCAGTTGCTCACCGGATCCAACCGGT  
 AGAAGGTGCGCGAGCGCTCGGATTGGTCACTGGGATATGCCGCTCGGGACGGTCAGAGCCCTCGGTCCGCCAGCA  
 CTCCGCAGGCTTCGTCGGGTGGTCGCGACGCGATGGCACCATCGATTCAACCAGGTCGCGGAATCACCAGCA  
 CGTAGACGGTTCTTCTTAAGCAACACCGAAGTTCAGGACCGAATGCTCCGGAAACATGTCA

:::::::Rv29T7.seq:::::::  
 CAGGCATGCAAGCTGATGCCGCCAACCGAGCGTAGCAGGCCGCCAGCCACCACGCCGGTCCGGCGCCGGCC  
 CGGGCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCGCGCACACCACCCGGCTGCGCTACGTCGAGCCATACCGG  
 CGGGAGCTCCATCCGCTCGGCCAGTGTCCGGCC

## Clone Rv2

:::::::Rv2SP6.seq:::::::  
 CCTGCATCCGGCTCGTATGTTGTGGAATTGTGANC GGATAACAATTACACAGGAAACAGCTATGACCATGATTA  
 CGCCAAGCTATTAGGTGACACTATAGAAACTCAAGCTTCAATCCCCCTGCCCTGATACGCGTCGGCAACCGTGAA  
 CGCGATCTCGCGACCGCTCGGATCGGTTCATCCCGCACAAAACGCCGTCCGCTACGGGTGCGCTTCGCGTGT  
 CACCCAGACGAAGTGGTCGACGTAGTCGACTTCCGACAGGTAGTGCATCAACGCCGGACTGGAAACACNAGCCGACAT  
 GAACCGTCGATACAGCGTCTCNCGGAGAACTGGATGTGTCGACGGTCCGCTCGGGTCAACCGGGCAGCACGGG  
 GCGTAACATCAGTTGAGTCCCGTCGGCAAGCCGTACCGGAATCGGGAGACGA

:::::::Rv2T7.seq:::::::  
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 GATGGCGCGCAACAGCGCCGTATTCCCGCGCCGCCACCGCCATCCGTACGGATCACCACCAACGCCGG  
 CTCGCTAGGGTCCCGCCGGCGAGAACGTTCCGCGGTATGCCCGAGCACGCCAGCCGACCGCCGGATCTGCTTC  
 GGCGCACTCAGCCCTTGATGTAGTTGGCTGACCAGCGTGCACAGCGCGTGTGCGGGTGTGCGGAGAGTTCA  
 GAGCCTGGCGAAGGGGCCGCCAGGCCGGCCAGCGTAGTCGACGGGCTG

## Clone Rv301

:::::::Rv301SP6.seq:::::::  
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 GATGCCGGGATTCCAGCCGACTAGGATGTCTAGCCGGCCAGCCGCTGCCGCCGACTCAGGGATGTTCGGTATACC  
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:::::::Rv301T7.seq:::::::  
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## Clone Rv302

:::::::Rv302SP6.seq:::::::  
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 GCAGCGGAACATCGCCGCGGGCTGCAGCGTGAACGTCGAATACGAGTCGAACAGTGTGGCGCTAAAAACCCGAGC  
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 TNTCGGGGACCTCGCGACCCAN

## Clone Rv303

:::::::Rv303SP6.seq:::::::  
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 GAGCATGAGTCGGGACCGTGTGTCATGGTCGACACCCACGACGGAAAGACGAGATCGCCGTCAAGCNTGTGTGCCG  
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:::::::Rv303T7.seq:::::::  
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## Clone Rv304

:::::::Rv304SP6.seq:::::::  
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:::::::Rv304T7.seq:::::::  
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## Clone Rv306

:::::::Rv306SP6.seq:::::::  
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:::::::Rv306T7.seq:::::::  
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## Clone Rv307

:::::::Rv307SP6.seq:::::::  
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:::::::Rv307T7.seq:::::::  
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## Clone Rv308

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:::::::Rv308T7.seq:::::::  
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## Clone Rv309

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 TCAACCAAACCTGAAGGTGATTGTTAACCTGGG

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## Clone Rv30

:::::::Rv30SP6.seq:::::::  
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Clone Rv310

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GTCGAGGAACACGACACGAGCCGTACGCCGGCGTAAGCCGCCCCAGGATTGGCGAAAAACCGTTCTACGTGGCG  
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Clone Rv311

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CTGCCACCANACNATGGAGCCACTCGCCGGAACTGAAACGTGACCATACACAACGAGCCCNCCCTGACCGAAGAGTC  
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GCTTCGACGGTACGGTACCCATGATGGCATCCAGTTGGCATCGGTGAGCTGATAGATGCCAGCTGGTTCGCCAAC  
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Clone Rv312

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Clone Rv313

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ATTGCGTTACGCTTCCGGGTCGATTGCTGATGCACTGCCGAAAACGCGGATATGATTGTTGAAACCGTATCTA  
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 CGCAGCATGCACAAACGCGTACACCGCTGTACCAAGACGGCACCAGCAATACCAGCATGACGGTACCCACGAGGTG  
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Clone Rv314

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Clone Rv315

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Clone Rv316

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:::::::Rv316T7.seq:::::::  
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Clone Rv317

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:::::::Rv317T7.seq:::::::  
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Clone Rv318

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Clone Rv319

:::::::Rv319SP6.seq:::::::  
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 ACGCTGAAGTTGGTGTCTCCATGGACTTGGGATGTCGCTGACCGGTTACCTACNACTCAAGCTGGCGCGTCT  
 CGTCCGAGGTGCTGCTGCGATAGCCGGAGGCCGGATCCGAATGACGGATTCCNTGCCANCCTCCGAGTGC  
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 CGCGTCACTATTAAACCCACCCGGACTTCACTTCCACGACCCGAATGGCGCCGGTATTGATCATCTGCGCACCG  
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Clone Rv31

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Clone Rv321

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Clone Rv322

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GATGCCGGGATTCAGCCGCACTAGGATGTCTAGCCGGCCAGCCGCTGCCGCCGACTCGGGATGTTGGTATACC  
ANCGATCGGCAATCTTGCATTCGCCGATGCTGAACTGCTANCCACGCCAACCAACCAACTGTGACNACAATGCCA  
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:::::::Rv322T7.seq:::::::  
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Clone Rv327

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AACCTATTGCTGTGAGCTTCATTGCTGCGAGCAAAACAGTTGGTCCGGCGTTAGGAACCTGAAATTGACACTCAACCGA  
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Clone Rv328

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CTCAAGCTGGGGTGGCGCTGCGGTGCTGGTCTGGCGCGTGGTATCAACACCGCCCACGAAATGGGGCACAAAG  
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CGTGGCCATCACGTCGGGTGTCACACCGGAGGACCCGGCGTGGCGCGGTTGGCGAACGTTGGAGTTCCCTG  
CCCCCGAGTGTATCGGCGGTTGCGCTGGCGTTCAATTGGAGGCCAACGGCTGCGTCGGCTGGCGTCAGCCCC  
CT

:::::::Rv328T7.seq:::::::  
GCACCAAGGCCCCCACGTCACCCGTGACCTCCTGCGCCGACCCCGCCGAGGTCTGGCGTTACCACTGAAACGG  
GCGAGCGGGAGTCTGGTACGACATCGAACAAAGAGCAAGGTGCAAGGGAGTTGTCGCGCCACTTCGTCGATGACG  
GGGTCNATCCATTGAGGTCCGCGTGGCGTGGTCAACTCCAGGTACTCGACCTCACAGACGAGA  
GGACTCGATCCCACAGATCTAGGTGAGAACAGATCTTCTGTCGA

Clone Rv329

:::::::Rv329SP6.seq:::::::  
TCGCCTCGCATATGGTCACGCCAACGGGTCCGGATTCTGGGCTTCATCGCTCGCGCCGTCGGACAAACAGCG  
CGGTCGAAACCGACACTCGTTGTGATGTCCAGCTATCACCTCGTACGCCAACCTACNCGCTATCTCA  
GCCGCGATCTCCAGGCTCCGCCGAGCCAGGTGCATCCGGTCCGGATCCACTAACCGGCACCATTGGCGTCN

:::::::Rv329T7.seq:::::::  
GTCCTCGAGTGCCTGGCGCCGTCGNACNCCCAGCGCCCGCGCCACCTGGATGCGACCCGTTCAAGTCCCTTCATCAT  
CTGCGAAAAGCCTTGACCCATGGCTCCGCCAGGATCGCGAGACCGGGCACCCGGAGGGTGTGCGAACGACAGCTCGCA  
GGATTGCGCCCTGTAAACCCAACCTCGGCAAGTCCCGCGACACCGTGAAGTCCCGGCCGGGTTGACGAGCACGAT  
CGACATGCCCTGGTGCCTGGCGGTGTCGGTGGCGT

## Clone Rv32

:::::::Rv32SP6.seq:::::::  
 GGCATACCAATGTGGACTTCTGTCACCCACGATATCCGTGGTCTGATCCGCTGCTGC GGCGGGCTGCNACCTGCNTCTCNGCGCACCGTNACTACATGGCNCGCGCGCACGCATACGTCGCGGGGGACCCACTCCNACTGGTCGACGGTGC  
 TGGCCCGTGTCCGCAAGTCCNAACCCGGCCGACCGACGAAACCGGCCGTCCTCTGGACCAACGCTCATGTC  
 GCCGTGGGGTCCATGCTCGACGCCATCGAGACCGTAACCAGCGTCCTCGAGCGGTTGCCTCCGGCTTCCGTGACAT  
 CTTCGTGGCTGTCGCGCGTGC CGCCGCGGATGGTCGACCACAAACGCCAACCTCGGCGGTGACATCACC GTC  
 CGCGCACTCGACCTGGCGCGATCGCGGCC

## :::::::Rv32T7.seq:::::::

GTGAGCAGACCTACGCCNCCTGGTGCGCCAACCTGGTACCGATCATGGCGCNGCCTGTCGTACCGATACCCAGC  
 GAACAAGACAGCCCGTCCGCGACAAGATGACTTCCCAGTCTTCGGCAGTCCATGGGGTGTCCGGAGTCCCC  
 GGCGCCACCGCGAGGTAAACCTCGTCTCAGTCCCACAGCGACCGGGTATCCACGTCGCGAACACGCCACCACCTC  
 CCCAGACGCCNCGTTGTACGCGGCTGGGTCACNGCAATAAGTGGCCTCANGGCATCGTCCGGCGGTCCNCAAC  
 GCA

## Clone Rv330

:::::::Rv330SP6.seq:::::::  
 CTCAAAGCTTGAGGTTAACTTGAACGGATCGAGCTGGACGGT GATCGGGCGAACCTGAATTGTCCGGT  
 AATGCCAACGAAAAAGCAGGGTGGTGGCCGGGGCGGTGAAACCGGGTCCGGCAGCCTGCAAATCTATGTGGAT  
 TGCGGAATGGGGATGTCCGGCACGGCAAACCGTAGTTGCTGTCCGTGAGGCCAGGTGGATGGGGGGAAAGAT  
 CCTGGTGTCCGGGATAATAATGGGCCGATGCCGGGTTGAAGTCCACTGGATCGGAATTCCGGAATCTTGATCCG  
 ACGTTCAGGCCAACAGGCCCTC

## :::::::Rv330T7.seq:::::::

CGGCGACGTCGCGATA CGCCGAGCAGTTGGAATCGCTCTGCAGCAAACCAATATTCTGCGCAGCTTGAGAGGACT  
 TTTTGAATGGACGGATCTACCTGCCGCGACGAGCTGGACCGATTAGCGTACGCCCTCCGCGTGGACGACACCGGGG  
 CACTCGATGACCCGACGGACGGCTCGCCGCNTGCTGCGGTTAGTGCACCGCGCAGACTGGTNTTCGCTGG  
 GACTGCGGCTGATTCCACACCTCGACCGCCGACGCCCTGCTGTGCGGCCATGTCTGGCATCTACGCCGTCAGC  
 TCGCCTGATCAGACATGCCGGCGTGTCTA

## Clone Rv331

:::::::Rv331SP6.seq:::::::  
 CTATAAAATACTCAAGCTTGATGCCGCCAACCGAGCGTGAGCACGCCAGCCACCGCGGGGTGGCGCC  
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 CCGGGCGGAGCTACATCGGCTCGGCCGCCAGTGTTCGGGCCCTTTCGAGGTCNAGGTCNATACCGATTGCGCAT  
 CGCAGCCGACCCCTGAACNACANAACCGTGCCTACTATTGCTTGTGCNGCGGGGCCAAAAAACAGCTTGGCATTCC  
 GGCCNATTGGCGGCCGCG

## :::::::Rv331T7.seq:::::::

CTTCGGTCGAGTGTGCGAGTGATAGATGACGACGGGACCTCGTCGGCATCTTCATAGCCGCCACACCTTCAGTT  
 GCTCACCGGAATCCAACCGTAGAAGGTCGGCGAGCGCTGGCATTGGTATCGGGATATGCCGCTGGGACGGTCAG  
 AGCCCTGGGTCCGCCAGCAGTCCGAGGCTTCGTCGGGTGGTCGCGACGCCATGGGCCACCATCGCATTACCA  
 GGTCTGCGCGAATCNCCANCACGTANACNGTTCTTCCTAA

## Clone Rv333

:::::::Rv333SP6.seq:::::::  
 CTGGCACCAAGGCCCCACAGTCACCCGTGACCTCTGCGCCGACCCGCCAGGTCTGGCGTTACCACCGAAC  
 GGGCGAGCCGGGAGTCTGGTNCGCATCGAACAAAANAGCAAGGTGCATGGCGGAGTTGTTCCGCCACTCGTCGATGA  
 CGGGGTCNATCCATTGAGGTCCGTCGCCGCTCGTCAGTGGCGGTCAACTCCAGGTACTCGACCTCACAGACNA  
 AAGGACTCNATCCCATCTAGGTGTGGACNAAACAGATCTTCTGTCGACNACTACACCAACCCAGGCCATCGCCGC  
 CGCCCGGATGCCAACCTCGACGCCGTACTGGCCCCGGCGGGGGCGCTCCCGGTTGTCAACACTTGCCTGTCNT  
 TCACGCNCTGCCAACATCCAACCCCAACG

## Clone Rv334

:::::::Rv334T7.seq:::::::  
 GTTCTGGGCCATGCGGAGGTATGCCGTTCCACCGCGGTGGGGTGGCGTTGCATTAGCTACCGATGGTGC  
 CTTGTGCAGGCCGCCGGATACCCCGAGTGCGGTAAACCATTTGTGCTGC

## Clone Rv335

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:::::::::::::Rv335SP6.seq::::::::::::
CAATACTCAAGCTTGGCGTGCCTCAACCCGAAATGGCTTCCGGGCCATCGGTAGGGACGGCGTGCAGGCTCA
ACNACNACGTCGTCGCCGGGACACACCTCGATGCTGCCCATGGACCGGGTCAACGCAAGCAGCTGATCGAGCTAC
AACGCCGCCGGAACGCTTCCGCCGGCGTACCGCATCCCGTTGACCGGGCGGATC
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:::::::::::::Rv335T7.seq::::::::::::
CNCATGATGATCATCACCCGAAAGTGTGGTAGCCGAGTGGTATCGTGGTACCGTCGTGCTTCATGGCGCCTC
TTTCGGGCTTCCGTATTGGCTTGGCAGGACATTCTGGGTATCGAGTTACTGGATGGTGTGGCGATGTCGGTGT
CCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGATTCGGTGAAGAGAGAAATTGGGCGGATTGAA
CACCGGAATTATCCGTGCCATGGTACCGGGGAGTGGTGACGGCTGCCGCATGGTGTTCGGTACCATGTC
GTTGTTGTGTTAGCGATTGCAATTATGGTACAGTACGGTACAC
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## Clone Rv336

```
:::::::::::::Rv336SP6.seq::::::::::::
ATACTCAAGCTTACGGTATCGNCATCACCTGGTATGAACCTGGGCTACGTGACGGCGCAGCGCAGCGCTTCTT
CGGCCGCAACATGCGCCAGTCCGCTACGTNACCCCTCCGCAGTGTCCATGGACAACAGCGCGTT
CTCCACCGACCGGGCCGGGTGGGGTNTT
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:::::::::::::Rv336T7.seq::::::::::::
GCTGGTAGAGTCGCTGACCGGTGACGGTTTGACAATGTGGTGCCTGGCGCTACGTGCCATCGAGACACTGGC
GCAGGCTATCGCACCCGTTATCGCTACGAGCAAATCGGGTATGCGTTCTGAGCATGAGTCGGCGACCGTGT
GGTCGACACCCACGACGGAAAGACGCAGATGCCGTCAAGCATGTGTGCCCGATTATCAGGACTGACCTCTGGCT
GACCGGCATGTTGGTCGCGATGCCGTGGCG
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## Clone Rv337

```
:::::::::::::Rv337SP6.seq::::::::::::
GCTTCCGCCATACCCGCCATGTCNCGCACATCCAGGACTCTGGGGGATCCGCTGACAGCGGGGGATCCCAAAG
TGCAGGATGATCGGGCGCCTACGTCGTGGTACCTCGTCAACAAACGAAACGAGCTATGACTCGGTACACGC
GGTGGCGCACATGGTGGACACCACACCGCCACCGCACGGGCTATGTCACCGGTCCGGCANCACTCAATGC
CGACCAGGGCGAGGCCGGANACAAAANTATCGTAAGGTACCCGCGATCACNAGCATGGTATCGCAGCAATTTGCT
AGTGTATCGTCCGTAAATTAA
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:::::::::::::Rv337T7.seq::::::::::::
CTTCCAACCCGAATTGGCTTCCGGCCATCGGTGAGGAACGGCGTGCCTGCAACGACGACGTCGTCCGGGAC
ACACCTCGATGCTGCCGCCATGGACCGCGTCGAACGCAAGCAGCTGATCGAGCTACAACGCCGCGGAAACGCTTCCG
CCGGGGCGTACCGCATCCCGTTGACCGGGCGATCGCGGTGATCGTCAACGGCATGCCACGGAGCGACGGC
CAAGGGCGCGTGCACGTCGCCGGGCGACGGTGGTGGCTGGCGGTCCGATCGGCCCA
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## Clone Rv338

```
:::::::::::::Rv338SP6.seq::::::::::::
TACTCAAGCTCGAGATCCGGATGGCACTCACGCTGGACAAGACCTTCACAAATCTGAAATCTGACCCGATACT
TGAACCTGGTCTCGTTCGGCAATAACTCGTTCCGGTGCAGGACGCCGAAACGTNCTCGCATCACGCGTCCG
ANCTGAATTGGCAGCAAGCGGCCGCTGTCGGCGCATGGTCAATCNACCAGCAGCTCAACCCGTA
```

```
:::::::::::::Rv338T7.seq::::::::::::
CCCACGACTTCTCCTCGATCAGTGGATTGATCGAAAGAGGCAACGAAAGCAGTGTACCTCGGGATGGTCAGCGCT
ACATCGACCCGCCGTTCACGCCACAGCCTGCTAGATCGCTGGCGAGCAGGCTCCACAGTTCGCCGCTAACGGC
GGCGTGTGTTCCCGTCCGGATGCCATTGCCCTGGCGTCTGCTCCATTGATCAATAGGGCTGGCAGCTCCGTC
GGCAGGGGCGTACGCCCTACCCGTCACCG
```

## Clone Rv339

```
:::::::::::::Rv339SP6.seq::::::::::::
CTCAAGCTTATGCCGCCGGCGAGGTCTGCTCACGGCAACCCCTGAAGTTAGGGACNACCTACTCAGCGCAAAT
TTCGCTAATGTGAGTCCGCCCCACAGGGGNANATCAACCCATGCGATCATGATCTACCCGGATACGGATTGGCGG
TAGCGCCCACGATCGTCAAATNTCCGCTGAATCATGGATAGCTGATCCGGCGTCAACCGTTTGANTTCACCGC
GCAACAGCCGCCAGGCCGGCCGANCAGCGATCTCNGGCCATGGCCCCAATCTNTCG
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:::::::Rv339T7.seq:::::::  
 GTGTGTGGTGGAACCCATCTGAGCAGTGTGCCAACCGGGGAGACAGCTCCAATTGACGTGAGCCGCTCACTTGC  
 TGGGTAAGCGTC

Clone Rv33

:::::::Rv33SP6.seq:::::::  
 CTTTACACTTCCTGCATCCGGCTCGTATGTTGAGCGGATAACAATTACACAGGAAACAGCTATG  
 ACCATGATTACGCCAAGCTATTAGGTGACACTATAGAATACTCAAGCTTGGCGTGACGCCACCAGGGCACTCCG  
 CACCATCTGTACCCGACCAAGATCTAC

:::::::Rv33T7.seq:::::::

CAGGCATGCAAGCTTAGCTGCCGAATCGTCACCCGATGCCAGATCGGGCTTCGCAGATAAACGACGAACA  
 GGCAGGCAAAACGTCNATCTGGAGCCGAAGGGCAATCAGCCGACCGTCAGCAACGACACCAGGAGACCACTTAG  
 GCAGTGACGGCGGGCCGAACATTACGCCCTCGTTGATTAGGCCTCGGTCTCGTCCGGTCAATGCCGAGCAGCTTG  
 CGGCAGATCTGAACGCTGTCCCTGTCCGGGAGCGGGCCGGCGTGGGTGCTGCCAATGTGACGAAACGGAGC  
 CGGACCCGTCTGGCGGGCCGCGGACGGCGATCCGC

Clone Rv340

:::::::Rv340SP6.seq:::::::  
 CNCAAGCTTGCAGATGTTACCCCTGACAGCCTGAACATATGTCNAACACACGGCACCGAACGGTGTGGGGACCCC  
 ATCGANTTCGAGTCGCTGGCGCCACTTATGGCCTGGTAAAGGCCAGGGCNANAGCCCGTGCCTGGGTGGTC  
 AAAACCAACATCGGCCACCTGGAGGCGCCGGTGTGGCTGGATNCATCAAGGCGGTGCTGGCGTGCAACGTGGG  
 CACATTCCCGCAACTGCACTTCACCCGGTGGAACCCGCCATCNACCGTCCGCNAACGGCTGTTCGTGCNACC  
 NAAAACCCCCGTGGCGCGCGC

:::::::Rv340T7.seq:::::::

GGAACCGGTAAACAGATCAGCTCGTCACTGCCGGGGTAATTCCCCACCGGTGCTGCCGCTGCCAGTAG  
 TGCACCTTCTTGACGCCCTCGAAAAGGGGAGTCGGTGGTAGGTACCGTCAGGAGCCCTACCCAGGTTGGCGCNA  
 TAGCCGGTCTCCTCGAGTATCTCCCGCACGCCACCGGTGGCTCACCACATTGCCCCTGGCAGC  
 GACCAGTCGTCGTANCNGGGCGGTGAATGACAACGATCTGACCGGCCCTCCN

Clone Rv341

:::::::Rv341SP6.seq:::::::  
 TACTCAAGCTTCAGAACAGGCCTGTTGTCGGCNACCCGGCTGCCGAGTTCTGCACGCCACGCCCTCAAGTGGGGCCC  
 GCACCGCCGGCATCTCCGGTCACGCAGGGCCGCCGGCGCCAGCGACGGCGTGTTCGCGCAGTCGCCGTCAA  
 TGATGCTGACCTGATCGGCCACCCGGCGTCTCGGCGTGTCCGTTCACTAATCGGGTGTCAAGCGTCTCGA  
 CAGCCACCAACCGAGTGCGACCAGCTGC

:::::::Rv341T7.seq:::::::

TAATGCTTGCCAACGTCACCCACAATCGCGATGAATTCAATCATGCCGCCAGGGCGGCCAACCCATGGTGGCGCG  
 AGCGGCAGCTCGATCGCAGCGGGAGGTTGCCGGGCCAGTTGATTCAAGAACAGGGTAGGTCATAGGCGGGCAGG  
 ATAGTGACGAAGGCAAGACCTATATCTGCCGTGGAAGAAGAATCGAGTAGCCGGTCAACAAACGAAGCGAAAGTG  
 TCCCGGATGTTGATGAGCGTCCGGTTGTGGCGGGTGGCGGC

Clone Rv343

:::::::Rv343SP6.seq:::::::  
 TACTCAAGCTTCGTCAGTTATCGGCCAGCAGACAAACAGAGCATCGGGACATACGGAGTCACACTACCCGCCAA  
 CGGTGATTTCCTGGCCGCCGTCAGGGCGCAACGACGCCAGCGACCACATCAGCANATGCCAGCGTGGGGC  
 CACGAGGTTGGTGTCCGGCGTACTCCAGGGTGGCGCGTGTACGACATCGTACCCGCCGACCAACTGCCGGCCT  
 CGGGTTCACCGCAGCGTGTGCCGCCGAGCGGANNATCACATGCCCGATGCCCTGTC

:::::::Rv343T7.seq:::::::

CCACCCGTGAATTGGGATGGCNAAAAGGCNAAGCAGCGTGGCCACGAACGCCGGAGGGACAATCTGGCGG  
 CTAGGGCTTCTCGCGGGAGGCCGAACGTAACGGCTTCAACACGTCGCGTCCGACCGCAACATTGGGG  
 ATGGCAGCAACCTGGTAGCACCCCTGGCGGGCGATGATCTGAGCGTCCGGTAGTCGCCGCCGGCGCTAC  
 AGTCTGAAACGCGATGACCATCGATGTGGATGAGCATCCGACG

## Clone Rv344

```
:::::::::::::Rv344SP6.seq::::::::::::
TCAAGCTTAGCTGCCGAATCGTCANCCGATGCNCCCAGATCGGGCTTCGCANATAAGCACNAACAGGGGGC
AAAACGTCNATCTCGGAGCCGAAGGGCAATCANCCGACCGTCNACAAACGACACCAGCGANACCACCTAGGCAGTGA
CGGCCGGCCGAACATTACNCGCTCGTTGATTAGGCCTCGTCCGGTCTGCAGCAGCAGCTTGCGGACANA
TCTGAACGCTGTCCCTGTCGGCAGCGGCCGGCTGGGTGCCTGCAGAATGTGACNAAACGGAGCCGGACCN
TCTCGGC
```

## :::::::::::::Rv344T7.seq::::::::::::

```
CCGGGGCCACTCCGACAATCNGTACCNACCAANATCTACACCATCGAATACGACGGCGTCGCCGANTTCCGCGGT
ACCCGCTCAACTTTGTGTCACCCCTAACGCCATTGCCGGCACCTACTACGTGCACTCCAACTAACCTCATCCTGACGC
CGGAACAAATNGACGCNTCGGTTCCGCTGACCAATAACGGTCGGTCCC
```

## Clone Rv346

```
:::::::::::::Rv346SP6.seq::::::::::::
NCTGGCCTTGGTCACACTAANACAATACTCAAGCTCCGGCCGAGAGCGCCAACTCACGATATCGTTAACCGAT
ATCCCGAGCCGATAGCTGGCGGGCTCGGGTGGCAGCGCGCTGCAGCNAAGGTGTGACCGTCATGAAACAGAC
ACCACCGCGGCCGTGGCCGTCGTCACCTGCTCGANATCTCAGCATCGCAGCCGGTGTGATCGCGCTTCGGCGTG
TNGTGGGTNCNCGCCGAGGCCGGCAAAGGCCGGCCACAAACCCCGGAAC
```

## :::::::::::::Rv346T7.seq::::::::::::

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CATCTGCCACCACACGGACCCGGTGCAGCGCCCTGACGCCCTGGTGTGAGCATCGTGGCCGGTCTGCTGTTG
TATGCCAGCTCCCGCCGCGCAACTGCTGGTGGCGCGGTGGTGCCTGCATTGCTGGCCTGGTGTGACCCAC
CGCGCGACGACACCCGGTGGGTGGCTGGGCTACGGCCTGCTATTGGCCTGGTGTCTACGTCTCGTTGTTGCCGTGG
ATCGCGAGCTGGTGGGCCCCGGGCGTGGTGGCACT
```

## Clone Rv347

```
:::::::::::::Rv347SP6.seq::::::::::::
GACAATACTCAAGCTTAGCTGGCACCCACCGCATGACCACCGACAGGCCGACTGGTCGTACCAACTCGAACGCCGG
GGTGTGATGTCCCAGCCGCTGAANTCGTCTGCGCGCGCAGGCCGTCNAACAGGTACAGGGCGGGGAATTGGCACC
ACCACTTGAATTGGACCTTGATGTCACGGCCATCGACGGCACGGCAGGTACTCCACCGCAAGGCCGG
CCGGAAAATGCCCGCGGTNCCTGCCCCGACGGCGCCGANCAAACCCGACACTAGGGCCGCCNACGGCCCC
GACCACNANTCAGCGACATACCGTGACGGCGCCACNAACCTGTCAACA
```

## :::::::::::::Rv347T7.seq::::::::::::

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CCTCCAACCTCGCGGGGAAGCGACNCCAGCCTACCGAGCTGGAGTCCANGACGCCAGCGCGCGTCGGTCTCGCTC
GTGGTGCCTGGGGTGGCGTTGGCTGGCAACGATCTCCACCCAGCCGGTGGTTACCCACGATCTGGCATANACG
CGGGCCGAGGCCGGTGCAGTACCGTATTGCGTCATTGGACGGGTTGTGCAATTGGCTAGCTCGTTGCCACACCC
GTCAGGGTTGACGTTGGCGGGTTCGGGGCCCCANACCGCTGTCAACCATGCCGCCAGCCGACCTGCGGCC
ACCAACTGCAGCACCACATGTCGCCGTGCGCGCCGATCACATGG
```

## Clone Rv348

```
:::::::::::::Rv348SP6.seq::::::::::::
CTCAAGCTTTGAGCGTCGCGGGGCANCTCGCCGCAATTCTACTANCAGAGAANTCTGGCCGATACGGATCTG
ACCGAANTCGCTCGGTGTCANCCACCCCTATTGGCGATGGCGCCGACNATGGCGCTGGACCAGATTTGTGCCGCTT
GCCGACGGCGACCGGTAGGTGGTCAAGTCCGGTCTACGCTTGGCCTTGCGGACGGTCCCACGCTGGTGGCGTT
GCGCGCNAAGCGCGGGTGGGTGCCATCAGGAATGCCCNCCGCCGCGCACTGCACGCCAGTGGCGCGCGA
```

## :::::::::::::Rv348T7.seq::::::::::::

```
CNCCAGCTTGATTGGTCTGGTTGCATTGGCAGCTGCGCAGGCCCTGGCTACCTCAACTACGACGACCCGAAACAAATT
GCCGCCTCGGATCGAGTTGGGTGGGTAACGCGGCAATGGAGCACCATTCTGGTGAATCAGACTATTCTGAGTA
CTTGATCATCCACTCTGCACACGACCTGCAACCCCGCGCGCCCTGGCAGCTGGAGCAGCTGGCGAACGTGTGAG
CCAGATCCCAGGCGTTGCCATGGTTCGCGGTGTGACCCGGCAAACGGGGAAAC
```

## Clone Rv349

```
:::::::::::::Rv349SP6.seq::::::::::::
CAATACTCAAGCTTAGCTGGGCCGACCTTCGGCGCCACCCACACCGTCAACGCCCGCAAGTCNACGTGTCAGG
CCATCGGCCGCGCTACGGATGGATTGGCGGGACGTGGTGTGACGCCGTCGCCGACCGAAACCTACCAGCAGG
```

CCTTCTACGCCCGCATCTGCCCGAACCGTTGTGCTGGTGGGTCCNACGCCGACATGCGCCTGGACATGCCGC  
TGGTCNACTTCTCTCACGG

:::::::::::::Rv349T7.seq:::::::::::::  
TCGACGGTTGGCGGCCCTAAATGCACTGAGGTGTCATTGACCCCACAGCGGAAATGCCGACTATTGCAGGCCTC  
CTTCGCCTTGGCTGCCGGAGAGGGGCTCCGCCGGAACCGCATGCAAGGTATATGACCTCGGTTCTCGGGTGCTACCGC  
GTGCCTTGTNTANGATNANCTCGCGTTGGATTGTCAGCCGGCAATTATCGAGCGCANATTGTACACNTGGC  
CGCGCGACATACGCTCACCGTGGATCTGCTCACACGGACGCCCTGCGGGATCCTGCTCACGGGTAAANGAAC  
TTACGTGGCACTCGG

Clone Rv34

:::::::::::::Rv34SP6.seq:::::::::::::  
GACCACGCCAGGCTAATCACGTGACGCTACCGAATACCCNCCTAGTGGTGCAGGCTCCGCTGGAAATGGCCCTGTA  
CCAACTCGCGCACCGGTGCCAG

:::::::::::::Rv34T7.seq:::::::::::::  
CGGCACCCGACCCCTTGAGCCGTCGCCGTGGCCCGGGTGGAACTGGCCGACGAGGGACTGATCGTGTGGCAAAT  
TGGTCGATGGCACGCTGGCGCCGATCTGAAGGTCN

Clone Rv350

:::::::::::::Rv350SP6.seq:::::::::::::  
CTCAAGCTTGCCTTACCCGACTTCCGGAGGGACACCATGAGCACCGCCAGCCGAGCACGAGGCCAAACTCCGCCA  
CGCAGGCCGGTTGGACTTGTCTGCTGGACAAGGGGTTAGCCGCCGAAGCAGTGACGTACATCGCGAAAAGCAGTT  
CGCCTGTCGACCGACGGNGCNNAACGTGAGGCTAGGGAAGCGAGGAGCACATGGCCGCCGACCCGCAATGTACACGCT  
GCAAGCAAACCATCGAACCCGGATGGCTATNCNTCACCGCCATCGCCGCGGT

:::::::::::::Rv350T7.seq:::::::::::::  
CATGTCGCGCACATCCAGGACTTCTGGGGGGATCCGGTACAGCGCCGGATCCAAAGTGC GGATGATCGGGCCGCC  
TACGTCGTGGTGACCTCGTGGTAACAAACGAAACCGAAGCGTATGACTCGGTCCACCGGGTGC GGACATGGTGGAC  
ACCACACCGCACCGCACGGGTGAAGGGCTATGTCACCGGTCCGGCAGCACTCAATGCCGACCAGGCCGAGGGCGGA  
GACAAAAGTATCGTAAGGTACCGCGATCAGGACATGGTATCGCAGCAATG

Clone Rv351

:::::::::::::Rv351SP6.seq:::::::::::::  
ATACTCAAGCTTCCGGTACGGTGGCGGGCGTGTGCTGGCCCGGGTGCAGCGCCGTGCGCAGGCTCGGTCTCGTTACN  
AGCTCGCGCTGCTGACACTGGCGGCNAGCCTGAACGGCGGGATCGTGGCCACCTCCCTGATCGTCGCGGGCTACA  
TAGCCGCGCTGGGAGCAGGGCCTTGCTGATCAAGCCGCTACTTGCACACCGGCCATCGCGTCATGCCGTGGAGG  
CGGTGCTGGGATCATCGCG

:::::::::::::Rv351T7.seq:::::::::::::  
TGTCAAGTCCTTCAGATCTCCTTTATGACATGACTGGAGATCTGCTAGATTGCAGCTCTGTGAGCGTGGGTAC  
CGGATTCAGCCGGTGGTCAGCCCGGGTGGTACCGCTTGCAGTGTCTGGCCCTCGAGTTCGCGATCGCG  
CGAAGTGCCTCGCGCAGCAAGATCGGGCGTAATGCCGGCATGACCGCGATGACCGCGATCCAGGAGAACCG  
TTCCAACCAGTGTGGCGGCCATCCGGCAAGTAGACCAAGTGCAGTGGTGCC

Clone Rv352

:::::::::::::Rv352SP6.seq:::::::::::::  
CAATACTCAAGCTTAAAACAGGCCTGGTGTGGCGCACCCGGCTCGCCGAGTTCTGCACGCACCCCTCAANTGCCG  
CCCGCACCGCCGCATCTCCGGTACCGCAGGGCGCGGCCGCANCGACGGNGTGTTCGCGCAGTTGCCGT  
CAATGATGCTGACCTGATCGGCCACCCGGCGTTCTGGCGTCGTNCGTTCACTAATCGCGTGCTC

:::::::::::::Rv352T7.seq:::::::::::::  
TACGCTGGCGCTGGAGGGAGCCANNTACAACATCCACGCCAATGCTTGGCCCGATCGCGCGACCAGGATGACCCA  
GGACATCCTGCCCGCGAAGTACTGGAAAAGCTCACACCCGAGTTCGTCGCAACCGGTGGTGGCCTACCTGTGACCCGA  
GGAGTGTGCCGACAACGATCGGTGTACGTGTCGGTGGTGGCAAGGTGCAGCGAGTTGCAGTGTGGCAACGACCG  
CGCCAACCTCGACAACCGCCGTCGGTACAAGATGTTGCGGCCGGTGGCCGAGATCACCAGTGTCCGGTGC  
AATTGCTG

## Clone Rv353

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:::::::::::::Rv353SP6.seq::::::::::::
GCTTTTCCCGTCGTCNNCGCTCAACCGCGTGAGGCCAAGCGGNTGGTTACGACTCCCTGTTGTGATGGACCACTT
CTACCAACTGCCCATGTTGGGACNCCCACCAGCGATGCTGGAGGCCTACACGGCCCTGGTGCCTGGCCACGGC
GACCGANCGGCTGNNNTGGGCGCTTGGTACCGGAATACCTACCGCAGCCGACCTGCTGGCAAANATCATCAC
CACGCTCGACGTGGTTAGCGCCGGTCAGCGATCCTCGCATTGGAGCCGGTGGTTGANCTGGAACA
```

## :::::::::::::Rv353T7.seq::::::::::::

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CNGCTTTTAATGCCCTGACNTGGCGNGCCGCCACCGGGGCACTCCGCACAATCTGTACCCGACCAAGATCTAC
ACCATCGAATACGACGGCGTCCGACTTCCGCGTACCCGCTCAACTTGTGTCGACCCCTCAACGCCATTGCCGC
ACCTACTACGTGCACTCCAACACTTCATCCTGACGCCGAACAAATTGACGCAGCGGTCCGCTGACCAATACGGTC
GGTCCCACGATGACCCAGTACTACATCATTGACCGAGAACCTGCGCTGCTAGAGCACTGCGATCGGTGCCGATC
GTGGGAAACCACTGGCGAACCTGGTCAACCAAACCTGAAGGTGATTGTTAACCTGGCTACGGGACCCGGCTAT
G
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## Clone Rv354

```
:::::::::::::Rv354SP6.seq::::::::::::
CTCAAGCTTGCCTGGGAGGGTGCATGGCCGACTCGGATTACCCACCANGGGCGCAACCGGGTGTCCGCGCCGTCNA
GCTGAACGTTGCTGCCGCCCTGGAGAACCTGGCGCTGCTGCGCACCCCTGGTGGCGCCATGGCACCTCGTAGGGACCT
GGATTTCGACGCCGTGGCGACCTGAGGTGTCGGGGACGAGGTGTCACCCGGTTGATTGCTCGCTGGCCTTGGCGGA
TGCCACCCCTGCGCCTGGTGGTCGATCCCGAAAANACGAANTTGTGGTGGAGGCTCTGCTGCGACACCCACNA
CGTGGTGGCACCGGGCAGCTTAGCTGGCAT
```

## :::::::::::::Rv354T7.seq::::::::::::

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CCGACGCCGTCGTGGCCACCAACACCGCAGCAGCACCGTGACCCGGACGGGGTGCCGCGAACCGGTCTGGCCA
ATTGCGCGGCACCAAGCCGTCGCGCGCCATGGCGAACAGCACCGGATTGCCCAGACATCAACACCATCACCACCG
TGGTAAGCCCGGCCAGCGCGCCAGGGAGATGATGCGCTGGCCCAGTACACCCCGTTGGCCTGGAACCGGGTGGCCA
GATTGCGGCCGCCGGCGGGCCGGTACGGTCCGAGTTGGTGTATGGAACCATGGCGACAGCACCCACCG
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## Clone Rv355

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:::::::::::::Rv355SP6.seq::::::::::::
TTNACTGGCCTTGGTCCACACTAGACAATACTCAAGCTTCCAGGACATCGTCATCGCGACCAAAACCGCGAGCTAGG
TCGGCATCCGGGAAGCATCGCGACACCGTGGCGCCGAGCGCCGCTGCCGGCAGGCCATTAGCGGGAAATTAGCCC
GCCCGGGCTCCCGCTCCGANTACGGGCCCGAATGGCGTACCCGGCTGGTAACCACGCTTGCCTGGCGCTGGCGCG
GCCTGCCGGATCAGGTGGTAATGCGACA
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## :::::::::::::Rv355T7.seq::::::::::::

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NGACGTCTCCATCCGCGTCGTTTGGCGGGTTGGCCACAGCAGCCGCCGGTGACGGCGACGATGCTGGGTGGT
TGCGGCCCTGCGCACCGCGCTTGCATGCTGGTGGCTGTCTGGACGATCCCAGTCCACCGGATCTGGT
GATTTGCGGGCTACCCGCGATTACCCCGCGCTCGACGAGTTTGGCCTGGACTACCCCGTGGCAATCTGCT
GAACTCGCGGCCGGTGGTGGCCTGGAATGTCGAGCGCCGTACCTA
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## Clone Rv356

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:::::::::::::Rv356SP6.seq::::::::::::
CTTCCTCTGAGTACCNCCGNTACTTGGATGGGAAAAAGGCGAATCNCCTTGGTCACGAACGCCGGAGGG
ACAATCTCGGGCGCTGGGCCTCTCGCGGAANGCCGAATGTACGGTGTCTCGACACTTCCNTCCCCCTCG
```

## :::::::::::::Rv356T7.seq::::::::::::

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GAGCATCGGGACNTACGGAGTCAACTACCCGCCAACGGTGATTCTTGGCCGCCGTGACGGCGCGAACGACGCCNG
CGACCCACATTCAAGCAGATGGCCAGCGCGTGGCGGGCCACGAGGGTGGTGCCTGGCGGCTACTCCCAGGGTGC
GCCNTGATCNACATCGTACCGCCGACCAACTGCCGCCCTGGGTTACGCAGCCGTTGCCGCCNAGCGGACGATCACNT
GCCCGCGATCGCC
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## Clone Rv357

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:::::::::::::Rv357SP6.seq::::::::::::
TACTCATGANCATCTTAATCANNGTTGCTTTTTATTAAATCTTCAATTACTGAAAGCAACAACAAAAT
CGCAAAGTCATAAAAACCGCAAAGTTGTTAAAATAAGAGCANCACACTACAAAGGAGATAAGAAGAGCACATACCT
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CAGTCACCTATTATCACTAGCGCTGCCCGCAGCGTGTAAACCGAGCATAGCGAGCGAACTGGCGAGGAAGCAAAGAAG  
AACTGTTCTGTCAGATAGCTCTACGCNCA

Clone Rv358

:::::::Rv358SP6.seq:::::::  
CTCAAGCTTCAGGTCATGTGCNCCAAGGCCCTGACGCTGGCCGACCAGGCCACCGCCGCCGGANACNCTGCCAAGGCC  
ACCGAATACAACAACGCCGCCAGGCCTCGCANCCAGCTGGTGACCGCCGAGCANANCCTCAAGACG  
CTGCATGACCAGGCCTANCNCGCANCTCAGGCCAAGAAGGCCGTCNAACGAAATGCGATGGTGCTGCACCANAAG  
ATCGCCGAGCGAACCAAGCTGCTCAGCCNG

:::::::Rv358T7.seq:::::::

CATGGTGGCACTGTAGCGACGCTGCTGCAATCAAGGTCATGCCGACTCTGGTCAGCTCGGANCCGCTGACACCCCGCT  
AAGGCTGCTCAGCTCGGTGCATTACCTCACCACGGCGAACCTCCCGAGCTTACGACTATCCGGATGACGGCACCTG  
GTTGCGGCGAACCTCATCATCAGCTTGGACGGCGGCCTACCGTCGATGGCACCAGCGGGCGATGGCCGGGCCGG  
CGACCGATTCTGCTTCAACCTGTTGCGTGAACCTTGCCGACGTCATCGTGGTCCGGTGGGACCGTGCCTGATTGAGGG  
CTACTCCGGCGTCCGGATGGGTGTCGTCCAGCGCCAGCAC

Clone Rv359

:::::::Rv359SP6.seq:::::::  
TACTCAAGCTTGCCTGGGTGATGCCCTGGTCAACGGCACCGTGATCGGATCGGGTCNACCGCACAAATGGACTGGAGC  
TTCGGCGAANTCATCGCCTATGCCCTCGCGGGGGGTGACGCTGACCCCGGGTACNTGTTGGCTCGGCACGGTGC  
ACCTGCACGCTCGTCTATCACCTCNGGCCACCGGAATCATTCCCGGGCTG

:::::::Rv359T7.seq:::::::

GTTGGNGCCTCGTCGGCGAACAGTTCTCGCACGATTCCGGATTAGCGGGACTGGTACCCAGTTGGTATGCGGGAG  
GCGCTGACGTTCCGGCGGATTAGCTGTTGATGGACGGCTGGTATGTTCTGATCACGGAACCTGGCTGTAATAGCCC  
AGGGTCGCCACGCTTCATCGGGGCCGGACCCGGCGACCGAGCGTGCAGGTATGCGACGTGATTTCGCTG  
AAGTCCCCGTACCCGGAGAACT

Clone Rv35

:::::::Rv35SP6.seq:::::::  
TGCTTCGGCTCGTATGTTGTTGGAATTGTGANCAGATAACAATTTCACACAGGAAACAGCTATGACCATGATTACG  
CCAAGCTATTAGGTGACACTATAGAATACTCAAGCTCCAGGTCAATGTGCGCCAAGCCCTGACGCTGGCCGACCAGG  
CCACCGCCGCCGGAGACGCTGCCCTGACCGAATACAACACGCCGCCAGGCCTGCAGCCAGCTGGTACCG  
CCGAGCAGAGCGTCAAGACCTCAAGACGCTGCATGACCGAGGGCTTAGGCCCGCAGCTCAGGCCAAGAATGCCGCTG  
AACGAAATGCGATGGTGCTCGGGATAAGATGCCGAGCGAACCAAGCTGCTCAGCCAGCTCGAGCAGGCCAGATGC  
ACGAGCA

:::::::Rv35T7.seq:::::::

CAGGCATGCAAGCTTGGAGGCAGACCCGTGCATGGTGGACTGTAGCGACGTGTCGAATCAAGGTCAATGCCGACT  
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AGCTTACGACTATCCGGATGACGGCACCTGGTGGGGGAACCTCATCAGCAGCTGGACGGCGCTACCGT  
ATGGCACCAGCGGGCGATGGCGGGCGACCGATTGCTTCAACCTGTTGCGTGAACCTGGCAGCTCATCG  
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Clone Rv360

:::::::Rv360SP6.seq:::::::  
TACTCAAGCTTGGGGTGGCGCTGTCGGTGGCTGCTGGTGTCAAAATCACCTCGCCCANACCTGCTACGGCACTTCTACATCGAGGACA  
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ACCGTGGCCATCACGTCCGGGTGTCACACCCGGAGGACCCGGCGTGGCGCGGTTGGCNAACGTTGTGGGANTTCC  
TGGCCCGCANTGTTATCGCGGGCTTGCCTG

:::::::Rv360T7.seq:::::::

GGCCATGCCACCGCNCCGCCCGAACGCTCAAAGGCACCTACTGGCACCAAGGCCACACGTACCCCTGTGACCTC  
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GCAAGGTGCAATGGCGGAGTTGTTCCGCCACTCGTCACTCGACCTCACAGCAGAGGACTCGATCCCACCTAGGTG  
TCGAGTGGCGGTACACTCAGTACTCGACCTCACAGCAGAGGACTCGATCCCACCTAGGTG  
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## Clone Rv361

:::::::Rv361SP6.seq:::::::  
 GCTTGGGGTATCGCCTGGTCAACGGCACCGTATCGGATGGGTCNACCGNCAGATGGACTGGANCTCGCG  
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 CGCTCGCAAGCACCTCNGCACCAGAACATTCCGGCTGGCTGCACNACGGGACNTGGTCNCCTCCAGGTCG  
 AAGGGCTGGGNAACAAANGCAGACCGTCCGACAANC GGACTCCTTCCGGCTTCGGCGAATCCGGACG  
 CCNAACCGACCGCG

## :::::::Rv361T7.seq:::::::

GTTCTCGCACGATTCCGGATTAGCGGGACTGGTACCCAGTTGGGTATGCAGGAAGGGCGTGACGTTGCCCGATT  
 GCTGTTGATGGACCGCGGTGGTATGNTGATCACGGAACTGGCTGTAATANCCAGGGTCGCCNCGTTCATCCG  
 GGCGCGACCCGGCGCACCGAGCGTGTGCGCAGGTATGCAGGTGATTTTCGCTGAAGTCCCCTGACCGGAGAACT  
 CGAACACGCTGAGGCCTCGTACCGTGTNNCGGACCAAGCGCGAGCAACTGCAGAAAATCGTTAAGANAGG  
 TCGAATCGTTGAAATTGGCACCACTGCACC

## Clone Rv363

:::::::Rv363SP6.seq:::::::  
 CACAAGACAATACTCAAGCCTCAGGTCAATGTGCNCAAGCCCTGACGCTGGCGACCAGGCCACCGCCGCCGANAC  
 GCTGCCAAGGCCACCGAATACAACACGCCGAGGCCTCGCAGCCAGCTGGTGACCGCCGAGCANANCCTNAA  
 AACCTCAAGACGCTGCATGACCAGGCCTTANCGCCNCAAGCTCAGGCCAAGAAGGCCGTCGAACGAAATGCGATGGTG  
 CTGCAGCANAATGCCGANCGAACAGCTGCTCAGCCAGCTCGAGCAG

## :::::::Rv363T7.seq:::::::

CCACCCGTGCATGGTGGCACTGTAGCGACGTGCTGCAATCAAGGTATGCCGACTCTGGTCAGCTCGGAGCCGCTGA  
 CACCCCGCTAAGGCTGCTCAGCTCGGTGATTACCTCACCGACGGCGAACTCCCCAGCTTACGACTATCCGGATGA  
 CGGCACCTGGTTCGGGGCGAACCTCATCAGCAGCTGGACGGCGCTACCGTGCATGGCACCGCGGGCGATGGC  
 CGGGCCCGCGAACCGATTGCTTCAACCTGTTGCGTGAACCTGCC

## Clone Rv364

:::::::Rv364SP6.seq:::::::  
 GCTTCGCCGATAACCCNCCATGTCCCGCACATCCAGGACTCTGGGGGATCCGCTGACAGGGGGGATCCAAAG  
 TGCGGATGATCGGGCCGCCTACGTCGTGGTACCTCGNCGGTAACAACGAAACGAANC GTATGACTCNGTCCACGC  
 GGTG

## :::::::Rv364T7.seq:::::::

CAACCCGANTTGGCTTCGGCCNTCGTGGACGGCGTGGGGTGTCAACGACGACGTGTCGCCGGACACAC  
 CTCGATGCTGCCGCATGGACCGCGTCGAACGCAAGCAGCTGATCTACNACGCCNGNGAACGCTTCNGCCGC  
 GGGCGTGACCGCNCCTCGTT

## Clone Rv365

:::::::Rv365SP6.seq:::::::  
 GGGATGGCAAAAGCGAACGACCGCGTGGCCACGAACGCCGGAGGGACAATCTGGCGGCTAGGGCTTCGCG  
 GGAAGGCCGAACGTACGGCTTCAACACGTCGCGCCCTCGACCGCGAACATTGGGGATGGCAGCAACCTGG  
 TAGCACCTGGCCGGCGATGATCTGCCAGCGTCCCCGGTAGTCGCCGCCGGCG

## :::::::Rv365T7.seq:::::::

CAGCAGACCAACAAGAGCATCGGACATACGGAGTCAACTACCCGGCAACGGTATTCTGGCCCGCTGACGGC  
 GCGAACGACGCCAGCGACCACATTCAAGCAGATGGCAGCGTGGCCGGCACGAGGTTGGTGCCTGGCGCTACTCC  
 CACGGTT

## Clone Rv366

:::::::Rv366SP6.seq:::::::  
 CTCAAGCTTACTGCCACCCACCGCATGACCACCGACAGGCCGACTGGTCGTACCAACTCGAACGCCGGGTGTT  
 GA

## :::::::Rv366T7.seq:::::::

TTGGTGGCCGGAAATGGCGAGTCCCATTANTCGTATTGTTAACAGCGACGAAACCGGTGTGAAAATGTCGCC  
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CGATGCCATTATGTGTTCTTACGCTNNNNNTCCGGTGCACATCATTATCTGCACCTTGCACTGCACATTGAG  
CTTAGCAGCGCTCG

## Clone Rv367

:::::::::::::Rv367T7.seq:::::::::::::  
GAATTNGCTTCGGGCCATCGGCCAGGACCGCGTGCAGGTGCTCAACG<sup>a</sup>CGACGTCGTCCGCCGGACACACCTCGA  
TGCTGCCGCCATGGACGCGTCGAACGCAAGCAGCTGATCGAGCTACAACGCCGCCGGAACGCTTCGCCGCCGGCG  
TGACCGCATCCCGTGTACCGGGCGGATCGNGTATCGTCACTGACGGCATGCCACCGGAGCGACGGCAAGGCCAAGGCCG  
GTGCCAGGTGCGCCGGCGCACGGTGCAGCAAGGTGGTGTGGCGTCCCGATCGGCCAGACGACATCGTGGCG  
ATTGCCGGGTACGCCGATGAAGTGGTGT

## Clone Rv368

:::::::::::::Rv368SP6.seq:::::::::::::  
TAAAGCTTCGTCAGTCATNGNGCCCCCGGACCAACAAAGCATCGGGACATACTGGAGTCAACTACCCGGCCAACGG  
TGATTTCTTGGCCGCCGCTGACGGCGCNAACGACGCCAGCGACCAACATTAGCAGATGGCCAGCGCGTGCCTGGCG  
GAGGTTGGTGTCTGGCGGCTACTCCCAGGGTGCAGCGCTGATCNACATCGTACCCGCCGACCACTGCCCGCCTCGG  
GTTCACCGCAGCCGTGCGCCCGCAGCGGACGATCACNTGCCCGATCGCCTGTTGGGAATCCCTGGGCCGCG  
TGGCGGGCTGATGAGCGCCCTGACCCCTCAATTGGGTCCAANACCATCNACCTCTGCAACACGGGACCCGATTG  
TTCGGACGGCAACCGGTGGCGANCACCT

## :::::::::::::Rv368T7.seq:::::::::::::

CCGGGAGGGACCATCNCGGGGCTNCGGCTCTCCGGAAAGGTTCTANNGTNNNNGCTTCNACNCTCCCGTCGC  
CCTGCGACCGCCGAACATTGGGTATGGNNGANCCTGTNAGCATCCNGGCCGGC

## Clone Rv369

:::::::::::::Rv369SP6.seq:::::::::::::  
CTCAAGCTTCGCACTCAGATCGTATAGAACCGGTGCCTCCACCGAGTGGCTGGTCGCCTCCAGCACGATCGT  
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GCTCATCGATACCGAGTGTGCTTTCCGACCACTCCAGTTGGTACGGCAGATTGACAAGGGCGTGAAGCCAG  
CCAGAGCAGGACGATACCNCGGCAAACCGGCGATTGCCG

## :::::::::::::Rv369T7.seq:::::::::::::

GCTTGGCAGCCTGGCGTGGCGCCCTNGAGCTTCGATCTGGATCTCCGGACTCGAGATGCTCACTGCCCGGCCG  
TGGACGTACCCATTGGCGCCGGACCCAGCGCCCAAGGTGACCGAGCTGGGCTGCACGCTGACCGGCCGCTCGG  
GGTCGACGCCGTAACGGTCAGCAGCTCCGANGTCCNCTGATCCGACCGCAGCTGCAATGCCGCTGGCAGCCG  
ACGTGGATGTGCCGGGCTAGATCGCGGGCAGCAGCAGACCGCGTACCGACGGTACACCTGCCAGTTNG  
GCCCTGCCGCAN

## Clone Rv36

:::::::::::::Rv36SP6.seq:::::::::::::  
GCTTCGGCTCGTATGTTGTGAAATTGTGAGCGGATAACAATTNCACACAGGAAACAGCTATGACCATGATTACGC  
CAAGCTATCTAGGTGACACTATAGAATACTCAAGCTTGAGCCATCGGGCTATCAGCTGGTGTGATGTCCCG

## :::::::::::::Rv36T7.seq:::::::::::::

CAGGCATGCAAGCTTGTGCTCTATCACATCCGACCAACCGCCCGACGGCTCGGCAGAACGCCCTCGCATATGGGT  
CGACGACCAAGCGGGTGGACTTCTGGGTGCGCAGCGCTCGGCCGTCGCACAAACAGCGCGGTGAAACCGACACTCC  
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TCCGCCCG

## Clone Rv370

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AGTCGCTGCGGTGCAAGCCACCCCTATGGCGATGGCGCCGACNATGGCCCTGGACCGATTTGTGCCGCTTGGCGA  
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## Clone Rv381

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CTCAAGCTTTACGGTGATCGCGCATACCTGGTTCATGAACCTGGAAAGCAGCGAGCGCTTCCCTTTCGGCCGAAACA
TGAGCCANCCCTCGTCGGCGTGGGTGCAGGTGCTCGGGCAGCTCGGCCGACAGCCGCTGACCTGAAACAG
CTTCCATATCCCGCAGACNAACGAC
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:::::::Rv381T7.seq::::::::::
CTCAGAAGLCGCTAGCTGGTAGAGTCGCTGACCGGTGACGTGGCGNCAATGTGCGCTCCGGTTCGCG
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## Clone Rv382

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CTCAAGCTTGCCTCATCAAGCGCAACAGCAGGGCGTCGGCTGGTCGCCATGACGGGTGACGGGACCAATGACGCA
CCCGCCTCGCGCAAGCCGATGTCGGGTGGCNATNAATACCGCACCCAGGCGGCCGGGAAGCCGGAACATGGTC
NATCTCCACTCC
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:::::::Rv382T7.seq::::::::::
ACTTCTATTCGACTGGTGTGCTGTGGCGCATCGACTGCCGGCTGGTCAAGGCCGCCAGTTGTGGATNCCACA
GGCAC
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## Clone Rv383

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:::::::Rv383SP6.seq::::::::::
GCTTGTCTATTCCGTGGCACTGTCAGACATATGCGCCGCTCCTCCTCATCGCTGCGCTCGGCATCGTCGCCGGCGGT
CATGGCGTCACCCCTACCCAAGCCGAACCGCAAACGAGAACGTGTCCATTATTAGGGTGTGACCAATACCAAGATT
GCTCACCAAGGAACCTCAC
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:::::::Rv383T7.seq::::::::::
CGATATTGTCGGCCGCGTTGTCTGACTGGTTCGCGT
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## Clone Rv384

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:::::::Rv384SP6.seq::::::::::
GACCTCGGCCACCAAGCCGACCGCACCCTCGAGGTCGATCCGGCTTGGCGTCAACCGCGTAAGGCAGACCAT
GGTCCCGGGCACGGCCANCCCTGCCACACGGCACTGGTAAGACTGCCCGTCTCGGGCN
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:::::::Rv384T7.seq::::::::::
CCGGAAGTCTAGGGGACGACCTACTCAGCGCAAATGTCGCTAATGTGAGTCCGCCCCACCAGGGCAGATCAACCCAT
GTCGATGACCTACCCGGATACCGGATTGGCGGT
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## Clone Rv385

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:::::::Rv385SP6.seq::::::::::
AGCTTCAGTCCCTCACGACCGTCTCCAAATGAATTCCCGATCCCACAATCTCGGTTCAAGATAAGGTGCCATAC
CCCTTACTCGGNAACGCTGGCGGATTGGCCCTGCCGCTG
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:::::::Rv385T7.seq::::::::::
CCGCCTACGGGTGCAACATGCATCCCGAGACCGATGCTCGAGCGCGACCCACTGCCGATGGCCGGAACCGGCTGG
TTACCCGGGTGGCGGCTGACC
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## Clone Rv386

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:::::::Rv386SP6.seq::::::::::
GCGGCTGGTTACGACTCCCTGTTGTGATGGACCACTCTACCAACTGCCCATGTTGGGACGCCGACCGCCGATG
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ACCTACCGCAGCCGACCCCTGCTGGCAAAGATCATCACCACGCTCGACGTGGTTAGCGCCGGTCGAGCGATCCTCGGC
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:::::::Rv386T7.seq::::::::::
GCCTTCCGCACAATCTGTACCCAGGACCNCTCTAAAAAATGAATACGACGGCGTCCGACTTCCGCGTACCCG
CTCAACTTGTGTCGACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAACTACTTCATCCTGACGCCGGAA
CAAATTGACGCAGCGGTTCCGCTGACCANTNNTGCGTCCACGATGACCCAGTACTACATCATCGCACGGAGAAC
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CTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGAACCCACTGGCGAACCTGGTTCAACCAAACCTGAAG  
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Clone Rv387

:::::::Rv387T7.seq:::::::  
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Clone Rv388

:::::::Rv388SP6.seq:::::::  
CTCAAGCTGCCAAAGAGACCTCGTCCACCAAGCNGGACGCGACCGTCNAGGTGGCGATCCGGCTTGGCGTCCACCCG  
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GCGGTTGGTGAAGGCGATGCTGCCGTTGCCGCGGGGGCGGATGTTGTCGGGAGTGACAATCTGATCGANAGGATT  
CAGGGCGGCTGGCTGGAATTGATGCCGCGATCGCACCCGGATCAGATGCCAAAGTCGGTCNCATCGCTCGGTG  
CTGGTGC

:::::::Rv388T7.seq:::::::

CCACGGCGTGGATCAAGGTACCGGGGATGTTGCGCAATGGCAGGTTGTTGCCCGGCTTGATGTCGGCGTTAGCGC  
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ACGCAATCCGTGCGGTACGGTACGGTCGGGTACTCGATGTCGCGACCTTGGCGTTGACACCATTTGTCATTGCGGC  
GAAAGTCGATCATCCGTAAGCGCCTTATGACCGCCCTTGTGCCGGTGGTAATCCGGCATGCGCTTGC

Clone Rv389

:::::::Rv389SP6.seq:::::::  
GGCGGCTGCGTCGGCGAGATGATGCCCGGTGCCACCCGATCCGTGCCCTGGTCAGCGCCAACGTGCTTCCGGTCC  
GGCGACCAACCATGTCGATGCCGAC

:::::::Rv389T7.seq:::::::

GCAATCGCCTTGGCGGTGCCGGGTTGTCACCGGTGATCATNCGGNGCGGATGCTCATNCGGCGATTCGTCNAAT  
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Clone Rv38

:::::::Rv38SP6.seq:::::::  
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GGCATCGCCAAGGTGGACTTCTGCTCAGCAGGAGATCCCGTGGTCGGATCCGCGGCTGCCGGGGCTGCGACCCCTG  
CATCTCGCGGCACCCGTGACCAAGATGGCGCGCCGAGGCAGACGTCGCGGCGGGACGCCACGCCACTGGCGATG  
GTGCTGGCGCGTGTCCGACGTCGCCGACCCGGCCGATCAGCAAACCGCCGCCGTCGTTCTGGACCTATGCC  
CACGTGCCGTCGGGTCCACGCTCGACCGACCGAGACCGT

:::::::Rv38T7.seq:::::::

CGCGTCCACCGCAGCGTGAGATTGGTGGCGCCATTCTCGCTGGTGAGCTGCTGTTGGCGGCGTCGCCGTATTGTGCG  
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GCCGCAACGGCCGCCCGGAAGCGTCTCGCAAGCGCCTATCCTTCGCAAGGTTCCCAGATCCTTCGCTACGTGGGTC  
GCTCATCGGCGGGCCGGCGAATGAGTACAGGTGAGGGTAACCGCTACAAATGAAGTGGTCAGTGCTGGCCAACGTG  
TGTAATGGTTGCCGGCTCGGTACACAGTACATTCTGGCAAGCGGGCAGATTGGTTCTCGCTCCTGGCCG  
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Clone Rv390

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TGTGCTGCAAGTTGTCGCCGCTGATGGCGACCTTGTGCGCTGATCACNATGACNAAGTCACCGCCATCGACATTGG  
GGCGAACGTCGGCTTGTGCTTGCCGCGAGCAGGTTGGCCGCCGACGGCAAGGGCCAANCACCACGTC

:::::::Rv390T7.seq:::::::  
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 TGGTAGCACCTGGCGGGCGATGATCTGAGCGTCGCCGGTAGTCGCCGCCGGCGCTACAGTCTGAAACGC  
 GATGACCATCGATGTGGATGCAGCATCCGACGAAACGGTCTACACGGGATATGTCGCTCGTGCGCCGGTG  
 GACCGGTGGTCTATCCCGGA

Clone Rv391

:::::::Rv391SP6.seq:::::::  
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 CATCATCCTCCCACGACGGCGCTCATCAGCTGGCCATTCAATGTACTTGATACCCCGCCTGCCGGTAGGCCA  
 CTGCNACAATTCAAACACGGTGTACACGGTGAATANTGTCNANATGGGCTCTGATCAACCGTCNCACCCGGTTTC

:::::::Rv391T7.seq:::::::  
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 ACCCGGATCATGGTAGCGAAAAGGAGATCGCCTGTCGATGCTGGATTGCCACCGGAGGCCATGACCGATTA  
 CTCGCCACCGGGGTGCGAGAGGGTGCAGTCCCGCTCCGTCACGCTCTCCGACGATCCATCCGGCTCCGCCGTGCG  
 GTGGCGTAGCCGTCGATGAAATGCTGCCGGCGCTACCACAAGGTGATTCTGTCGGTGTGCGAAGTGCCTTTC  
 GCGATCGACTTCCGTTGACCTACCGGCTGGGCGTCTGCACAAACACCCGGTGAGGTGTTTGTGCAAGTGGC  
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Clone Rv392

:::::::Rv392SP6.seq:::::::  
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 GCTCGCCGCACTGTCGCGGTTCANTGCCNACCGCGCCGCAACTGGTATTGCTGGACTGCGGTGATTCCACACCT  
 CGACCGCCGCAACGGCTGCCTGCTGCGGCCATGTCGGCATCTACGCCGTCNGCTGCCCTGATCAGACCATCGCC  
 GGCGGTCTGCTACCATCGCGAAATCTCTGTCGGACTGAANAANGCCAAGTGGCGGGCAGCACTGGNCTCTT  
 CGGTAACCTGCNGACCGCCATTGGACCGCTACCG

:::::::Rv392T7.seq:::::::  
 TTGATCTGGACGCTGAGACGGTATCGGNCCGAACTGAATTGTCGGTAATGCCAGCGCAGAAAGCANGGTGGT  
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 AAGCCGTAGTTCGCTGTCGGTGGAGGGCCANGTGGATGGGGGAAGGATGTTGGTGTCCGGATGATAATGGGCG  
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 CGGGTGGTGGC

Clone Rv393

:::::::Rv393SP6.seq:::::::  
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 GAGGACNAGGTACGAANCTCGCCAGCGGTGTCACCGCTCAGGGCGGATGTCGCCGTCGCCACCCGCGTACCGC  
 CCGATCGGACACCTGTATGACCGCGCGACNTGACCTGGGTGACGCCAACGGGTTTCAGGGCATNACNATCTCGCT  
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:::::::Rv393T7.seq:::::::  
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 TGACATTGCCGGCAGCGTCGACCTGGAAAAAGAAACGGTGATCACCGGCCGCTAGTGGACGGTGACGCCAGGGCG  
 TGGGCGCGCGTTCTGTCGCGCTGCTGGACNCCTCCGACGAGTTCACCGCCGGAGGTGTCGCGTCGCCACCGGG  
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Clone Rv396

:::::::Rv396SP6.seq:::::::  
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 CCAGGGAA

:::::::Rv396T7.seq:::::::

CGTCAGCACGGCGACGTCGCGNTACGCCGAGCAGTTACACAATCGCTCTGCAGCAAACCAATATTCTGCGCAGCTTC  
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## Clone Rv39

:::::::Rv39SP6.seq:::::::  
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## Clone Rv3

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:::::::Rv3T7.seq:::::::  
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## Clone Rv40

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## Clone Rv412

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Clone Rv413  
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Clone Rv414  
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Clone Rv416  
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## Clone Rv417

:::::::Rv417SP6.seq:::::::  
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:::::::Rv417T7.seq:::::::  
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## Clone Rv418

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 GACATCTGGCAAGTCGCTGGCAGTGACAACGCGATCAATGTGGTGACGCCACCGTGGCGCTCAAGCTGCTGC  
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## Clone Rv419

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 AACTGATATGTGCTCTGGACCAAGCAAGGACTGACATTGCCGGCAGCGTCTACCTGGAAAAAA

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 GCCTCCTGGGAAGCGGTGGC

## Clone Rv41

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:::::::Rv41T7.seq:::::::  
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## Clone Rv42

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## Clone Rv43

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GCTCCT
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## Clone Rv44

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## Clone Rv45

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Clone Rv46

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Clone Rv47

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Clone Rv48

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Clone Rv49

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:::::::Rv49T7.seq:::::::

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## Clone Rv4

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## Clone Rv50

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## Clone Rv51

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:::::::Rv51T7.seq:::::::  
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## Clone Rv52

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## Clone Rv53

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GAAGCGGACCCGACAGCCGTCGGGTATGGACTGATCGGATCCACCGGCATTGAGCCGGCTATCCGCGGGAAAGT  
TCGCCGGTCCCCCGCCACATACAGCGGAGGATAGGGCTTGTACCGGCTCGGCCAGCAGTAGATCGGATCGAAGT  
CCACATATGTCCCCATGGAATTCCGCCTGCTCCTGCGTCCAGATCTGATTATCGCGCGCAACCGCTCATCGATCACAC  
GTCGCCGCACCGCAGGGTCCACACCATGGTGGCAGCTTCTCGCGCA

## Clone Rv54

:::::::Rv54SP6.seq:::::::  
ATACTCAAGCTTGTGCGGGTAAACCCGCGAGCAGGGCGGTGGGTGCGGTGTCAAAAACAACCACACTTCTTGCGGTTC  
GGTGATCTCGACACCAGGCCGAGCCGACCCATGCGCGCTAAATCGGCGATCAGCGCCTGGCTATCGCCTGGGT  
GCCGCCACCGGAATCGGCAGCCGACCGAATGGGCAGCGTTGCCAGCATCAGTCCGGCAGGCCGACACCAGTGA  
CGGCAACGGTGAATCGGTGGCGCAACGCCGGTGAACAACCGCGGGCATCTCGCCCGCAGCGACCGCCAGGC  
AGGGGTGCCCTGGCCAGCATCCGAGCCGAGACCCAGGACCGAGCCCAGTGCAGTAGGCAAAGACCGCTTGTGCGGA  
GACATGAACCTCACGACCGT

## :::::::Rv54T7.seq:::::::

AGCTTATTGAACCGCGGGTGCAGGCAAAGTGGACCTCATAACGACTCGGGTCCAGCAGCGCCAAACACGAACGGC  
CGGACGACGTGGGCCAGGGTCGCGGCCCTCCCTACAAACAGGATCCGTTGCCGAGCGACAGGCTCGGTGCGCG  
TTGGCGCGTGTCTCGTCCCAGCGTCGGTCCCGGGTCGCCGGCAGCCTGTTCTCCATACTCGCCCCCTAACTCT  
CGAGGCAGCCCGTACCCGAGGCAACCTCCAAAATGCAATCCCCAAAATGCAATGCGTCAGGTATTTCTCACAC  
CGACCGCTAGTTGCGGATCAGAAATCCGTTGGCGCGGAAGTCCAGCCGAATTGTTCTCCGCTCCGATCATGCTT  
GTAATCGTTGGAAATTATCCTCATATGCCGATCGCTCATAGGGTCCAGGCCAACCGGGCA

## Clone Rv55

:::::::Rv55SP6.seq:::::::  
CTTCCGGCTCGTATGTTGTGGAATTGTGAGCGGATAACAATTACACAGGAAACAGCTATGACCATGATTACGCC  
AAGCTATTAGGTGACACTATAGAATACTCAAGCTTGGCCACCTCGCGGTGTGTTGGAACCCATCTGAGCAGTGTG  
CCAAACCGGGGAGACAGCTCCATTGACGTGAGCCGCTACTGCTGGTAAGCGTCG

## :::::::Rv55T7.seq:::::::

TAGCGCCCCCTCCGGCGGAGCTCACGGCGTGGATCAAGGTACCGGCCGGATGTTGCGCAATGGCAGGTTGTTG  
CCGGCTTGTGTCGGCGTTAGCGCCGGATTCCACACATCCCTTGCGAAAGTCCGTTGGGTGCAATGATGTAGCGCT  
TCTCCCCATCGAGATAGTGGAGCAACGCAATCCGTGCGGTACGGTTCGGGTGACTCGATGTGCGCAGCTTGGCGT  
TGACACCATTGTCATTGCGCGAAAGTCGATCATCCGTAAGCGCCTTATGACCGCCGCTTGTGCCGGGTGG  
TAATCCGGCATGCGCGTGCCTGCCACCGCAGCGACCGTGCAGCGGGCAGCAGCGACTTCTCCGGGTGACCGGGTGA  
TCTCGCGAAATCAGATACGCTGGCGCCGCGACGACCAAGCGTCGTGGCTTGTCTCGAATTGCGATGTCTAATCA  
GGTCTTCTC

## Clone Rv56

:::::::Rv56SP6.seq:::::::  
TGAAACTATATAACTCAAGCTTGCCTAAAGAACCTCGTCGACCAAGCAGGACGCCAGCTCGAGGTGGCGATCCG  
GCTTGGCGTCGACCCCGCTAAGGCAAACCAAGATGGTTCGCGGCCAGGTCAACCTGCCACACGGCACTGGTAAGACTGC  
CCGCGTCGCGGTATTGCGGGTGGTAAAAGGCCGATGCTGCCGTTGCCGGGGGGGCGATGTTGTCGGGAGTGACGA  
TCTGATCGAAAGGATTAGGGCGGCTGGCTGGAAATTGCGATGCCGCGACACCGGATCAGATGGCAAAGTCGG  
TCGCATCGCTGGGTGCTGGTCCGCGCCGCTGATGCCAACCCGAAACCGGACCGTACCCGCGACGTGCGCAA  
GGCGTCGCGACATCAAGGGCGCAAGATCAACTTCCGGGTGACAAGCAGGCCAACCTGCACTTCTC

## :::::::Rv56T7.seq:::::::

GCTGAGCTCACGGCGTGGATCAAGGTACCGGCCGGATGTTGCGCAATGGCAGGTTGTTGCCGGCTTGTGTCGGC  
GTTAGCGCCGGATTCCACACATCCCTTGCGAAAGTCGTTGGGTGCAATGATGTAGCGCTTCTCCCATCGAGATA  
GTGGAGCAACGCAATCCGTGCGGTACGGTTGGGTGACTCGATGTGCGCAGCTTGGCGTTGACACCATCTTGTG  
ATTGCGCGAAAGTCGATCATCCGTAAGCGCGCTTATGACCGCCGCTTGTGCCGGTGGTAATCGGCCATGCG  
GTTGCGTCCACCGCGACCGTGCAGCGGGCGACCCAGCGACTTCTCCGGGTGACCGGGTGATCTCGCGAAATCAGA  
TACGCTGGCGCCGCGACGACCGAGCGTGTGGCTTGTACTTGCAGTGTCTAATCAGGTCTTCTC

## Clone Rv57

```
:::::::::::::Rv57SP6.seq::::::::::::
ATACTCAAGCTTGTGGTGACCTGCCGGCGAACAGTTCTGCACGATTCCGGATTAGCGGGACTGGTCACCAGTTG
GGTATGCCGGAAAGCGCTGACGTTGCCCGCGATTAGCTGTTGATGGACGCCGGGTGATGTCCTGATCACGGAACGTG
GCTGTAATAGCCCAGGGTCGCCACGCTTCATCCGGCCGGACCCGGC
```

## :::::::::::::Rv57T7.seq::::::::::::

```
GATGATGCCGGTGCACCCCGATCCGTGCCCTCGGTACGCCGAACGTGCTTCCGGTCCGGCGACCACCATGTCGCA
CGCACCGACCAGGCCAACCCGCCGGCCACATGCCGTTGATGGCGCCACCACCGGACGCCGGACTCGACGAT
GGCGCGAACAGCGCCGTATTCCCGCCGCCACCGCCATCCGGTACGGATCACCAACCTCCGCCGGCCTC
GCTGAGGTCC
```

## Clone Rv58

```
:::::::::::::Rv58SP6.seq::::::::::::
ATACTCAAGCTTGCCGCAATCGAAACCAACCTGTTGTGCCGCAAGAAATTACGCCGTGGCCCGGCCGATCAAGAA
ACGCCCCGGCGCGCGGGTGCCTGCTGATGGCATGACGGGACCAATGTGACGCCATTGTCGAGCAGGCACCGGTG
CCAGCCCCGAATCCGGTGCACCAGGCACACCCGCCACACCCGGTATCGACGGCGCGTGTGTTCGCGTGTG
GCCAGCTCGCAGGACGCGCTGCCGAAACGCCGCGCGCTGGCGATTGGGTCT
```

## :::::::::::::Rv58T7.seq::::::::::::

```
TTGGCGGGTTGGCCACANCANCCGCCGGTACGGCGACGATGCTGGCTGGTGCAGGCCACCGCGGCTTG
CATGCTGGTTGGCTGTCTGGGACGATCCCGAAATAGTCCACGCGGATCTGGTATTTGCGGGCTACCCGCGATTAC
CCCGCGGGCTCGACGAGTTTGGCCTGGACTACCCCGCTGGCAATCTGCTGAACCTCGCGGCCGGTGGTGGCCTGG
AATGTCCANCGCCGTTCACGTGACCTTGATGGGATCCGGGGNT
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## Clone Rv59

```
:::::::::::::Rv59SP6.seq::::::::::::
NCGTGGACACCGGTGTCGANCGCCACCAGCCGATGTCGTCGANCCTCGCAACATCTGAATGCCGA
GCAGCGCCTGGCGTGTGATCGGCAACCGGGGATGACCGCTCGCCGATCCGCTCGACAATCCGGCGCACGTGACATGC
CGCGGACGGCTCGACGAGCTGGAACTTCAGCGACGACGATCCCGAATTGATCACCAGCACGGTGCTACTCATGGACC
CCTGCGCCTGAATCCGTGATGGCACGGTGTGACTATTGTCGACAGTGCACCCGAGATACTCTCACGGCTGCGT
```

## :::::::::::::Rv59T7.seq::::::::::::

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CATGTATTGCCGTGCTCACGGCGCCACGCTCGATGGTTCTCGAAGTCTCCGGCTGGTACAGCTTCTCGTTGATC
TCGTTGCCACGCGCTCTTCCCGCCGACGACCGGATCTCGATCTCCANAAATGATCTTGGCGCCGCCGCGCCTT
GAGCAGCTCTGGCGATGGCAGGGTCTCATCGATGGGACTGCCGACCGTCCACATGTGCGACGGAACAAAGATG
TCACCTTGCTCACCGCGTGCNCAGATNCANAAGGCCGGACATACTGTCNACTTGTCTGGCAGTGGTCCGTGTC
AGCCCACGTGACGGGTACTTGGCGCGATAACGTGGT
```

## Clone Rv5

```
:::::::::::::Rv5SP6.seq::::::::::::
GCCACACGACCCGGCCGTAACTCTGCTCACGAAATGCCGCCAGGCCGCGTAGCACGTGGTATCCGCCATAAAGG
TGCACCTTAAGCACGGCGTCCAATTCTCGAACGACATCTTGTGGAAGGTGCGCGCAAGATCCGGCGTGTGCTC
ACCACACCGTGCACGGCGCCGAATTCTGCAAGCGCGGTCTTGATGATGTTGCTGCGCCGTCCTCGGTGGCGACGCTG
TCCTTAGTTGGGACCGCCGGCCGGCCACCGAGGTGCGTGAAC
```

## :::::::::::::Rv5T7.seq::::::::::::

```
CAGGCATGCAACCTTGTCCACACGGCGTCACTCCGTGCAAGGTCCGACCGCTTCCACGTCCCCTGGTACGGTGCT
CCATCTCCCTCAGCAACGCGTGAAGTGGTCCGATCCCGGGCTTCAGG
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## Clone Rv60

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:::::::::::::Rv60SP6.seq::::::::::::
GTTGAGACGCAACCAGCGCACACGACGATTTGGCGTAGCGGGGACGTCGCTCGATTCGATCACGTCGCGCTCGCA
TCGAGCATGGCCCGCGACGCTACACGATCGCCGTCGATGACACGACGCCGAGCCGTACGCCGGCGTAAGCCGCGCC
AGGATTCCGGCAAAACGCTACGTGGGGGTGTAAGGGTGTGCAATGATTGTTGGGTGCGTATGCGTCTGCAAT
CGTCGACATAGATCCGTGCCGATCGCGTCGACAACCTCGGGGTGAGTGGAAATACACTTGCCGATCACGCGACGTGCG
```

CGGATCGATGCCGACCGAAATACGACCACATGGCTCTGTCNCAGTGTGGCGGATCAAATACCCTCAGTGCCGT  
CCGAC

:::::::Rv60T7.seq:::::::  
TTNCCGCCCTNACGCCACTCCNAGACGATGCTCGACCGTGTGAGCACACGGCGCTGCTGTAGACGGCACGGCGAG  
CTGGATCGCGCTTGGTGCACCCAAGCCTCTACCGCGCTCGCTCGTCATCGGGTACCGAACATATTCCGGTCGTT  
GCGCAGAGTGTGCATGTGCGGTCTTGTGAACGAACATAGCAAAGCGTATATGTCTGTGGCGGCTCTGCAGATATCGC  
GATAATACGTATATACATAAGGTGGCGCGATCTATCGGTATATCCGTTATGGCGGACGTGCGTACCGTGAGTCG  
GGCGATCGCGCACTTCGCGATCGGTACTGGTCCTCGGACTGCGCGATGCGTAGC

Clone Rv61

:::::::Rv61SP6.seq:::::::  
GGTGATGACGCACTGCTTCGAATGAGTCATTGACTACTCCCGTGGTTGTCTGCGATGGTGGAGTGCCGCGACGCT  
TGGCCGANGTCGCGATCGCGTCGCGGGCTCGGGGAGCAGACTGACCTGCAGATGGAAGTCGTGCCACATGCCCGGA  
ACGGCGAGCTCGATGCTTGTGTTTCGAAGNGCGCANGCGTTTCGATCTTGTCCGCGTCAACGAGATCGGATCTCGCC  
GCGGTCGATGACGATGGGCGCAGGCCCCGTCATGTCCCGTAGACGGGAGATAACGGGAGCCGCGGATCGAGACCT  
ACGTAGCGCGGCCCATCGTGCATCGACGAAGAATGACGGATCGCGCAGCGCGTCGCGTCTCGATGTCACGC  
GAGATGCCACGGCAGATCAGCGATGCGCGGGC

:::::::Rv61T7.seq:::::::  
CGGTACGCCGGCAACAAACGCCCTGTGACGAGCGCTCCGAGCGGTATGCCCTCACCGTCATGACAGCTCCTTC  
TCCAGGTCTACGCCGACGTCGCGGTCCACATTGGTGAAGCTGGCGAATGCCCTCGGAAACCTCGTCGAAATGCGCCTCC  
GCGTCCGCATCGAAGGTCGCCATGTCAGGATCAACTCGACGTAGTAGCTAGTACCGCATCAGGTCAAGTGTGTTGCTG  
GCCTCGGAGTCCGGCGAACATGCCATTCCCGACTCTAGAATCCAGTCATCGTCTCGGTGACGACGCCCTGCC  
GATCACATAGCTGACCGGATCGGAGAGAAATCTGGTTCTCGT

Clone Rv62

:::::::Rv62SP6.seq:::::::  
ATACTCAAGCTTAAGCGCAGCAGTACCGCGGTGCCTGGGCATCCAGCAAACGGGAGCTAACGAACGATTCTG  
AACGAAGGGTCGCCACCAACCTCCAAACCGAACGGTGCAGCCCCGGC

:::::::Rv62T7.seq:::::::  
GCAAGTCCGCTCAATGTGGTTGTGATCACANGACTACGTCGCCCTCAATCAGCTCAAACGTCAACCGTGGCGTGC  
GCAGCATGAAGGTCGGCGCCCGACGATGTGGCGAAGCAACAGGTAAATAACTGGTCGGCATGGTCAACCCCTATTG  
GGCGTTGCGGATCGGGTGCACGCCGGAGTGCCTCGAACTCAACACCGCCTCACCGATCTTCGTCGAAAATG  
GCGGTCGTTGCGGGTATACGTCGCCGATCCCACGAGGGCGGAATCCGCTGAGCCGCACTGA

Clone Rv63

:::::::Rv63SP6.seq:::::::  
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GACTTGAACGACCTGTACCGCAGGGTATCAACCCCNACNNNGNTGAAAAGGCTGATCGATCTGGGTGCGCCGGAA  
ATCATCGTCAACAAACNAGAANCGGATGTCGCGNGGAATCCGTTGAGCGCTGTTGACAAATGCCGCCGGCC  
GTCACCGGGCGGGCAACCGTCCGCTCAAGTCGTTCCGATCTGCTCA

:::::::Rv63T7.seq:::::::  
TGCCTGCGATGGCAGTTGTTGCCGGCTTGAGTCGCGTTAGCGCGGATTCCACACATCCCTGCGAAGTCGTGGGTGCAAT  
GATGTAGCGCTCTCCCATCGAGATAGTGGAGCAACGCAATCCGTGCGTACGTTGGGTGTAACGAGTCGCGCANCTT  
GGCGTTGACACCATTTGTCATTGCGCGAAGTCGATCATCCGTAAGCGCGTTATCGACGCCCTCTGTGCGCG  
GTGGTAATCGGGCATGCGCTTGCCTCACCGCAGCGTGCAGCGGGCGCACACCGACTTCTCGGGTACGGGTGATC  
TCGGCGAATCAGAACCTGGCGCGACACAGCGTGTGGCTGACTTGC

Clone Rv64

:::::::Rv64SP6.seq:::::::  
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CTGTTAAGCGGTACGTACTCCACGGCACTCAANGAATTANATCCGAATCGGAAACCCCTGGCAGCGTCGAGTCG  
CAGCGCCGTCGCGCCCCCACCCTCGCTCGGCATGCTCACATACCCACCTCGATCGCTGCGGGAGTTGCTCGTCGCCGAC  
CGACCGGGCAGCCGGCGAACACCGGAGGACCCAAAGATTCAAGCACCACATCGCTAGCCGATCTGGCGCGTGG

:::::::Rv64T7.seq:::::::  
 TCGTAGCGGTTGCACCCANTCCCGGACAGCTCCGCCACCGCAGCGACGGGATCACC CGGGTCAA ACC ACC CGAGCGG CGAGGATCTCTGGCCGTCGACGTGACCGCGCACGGCGGGTGTGGCCAGTCCCGACCGCCGTTCCACTTGGCGTAC GCGCTGGATGTGTTGTGCGCAACGGAATCCCACCTCAATTATGACCTCGTTGTGGCGAGCGCGGTATCGTACGCC GACCAGGAATCGTCACTGCTACCGTACCGAAGGCCTCTCCAGCACACCGCATCCAGAACGTGCACACNGTCG ACATGTCTCGCGGATCCGCGTCAAGAACGCCAGTGCCTGTGCGACACGGGTCGCGATCACC CGCTCGCACGC GGAGATCGGCACACCGCAGCGCATCGATCATATCTCGATCGGGTCTCCACCACCGAACAG

Clone Rv65

:::::::Rv65SP6.seq:::::::  
 ATACTCAAGCTTCGCTGAGGTGGTGGGGCACGATCACGTACCGCACCCTGTGCGTGGCGCTGGATGCCGGCCGGAT CAACACCGCGTACCTGTTCTCTGGGCCGCGTGGCTGCGGAAAGACGTCGTCAGCGCGTATCCTGGCNGGTCGTGAA CTGTGCGCAGGGCCCTACCGCCAACCGTGCAGGGGCTGCGAATCCTGCGTTCTGTTGGCGCCAAACGCCCGGCAG CATCGACGTGGTAGAGCTGGATGCCGCCAGCCACGGGGCGTGGACGACACC CGCAGGCTGCGGGACC CGCGTCTA TGCGCCGGTCCACTCACGGTACCGGGTATTATCGTCGACGAGGCGCACATGGT

:::::::Rv65T7.seq:::::::  
 GCACTCACGCTGGTACAAGACCTCACAAAATCTGAAATCCTGACCCGATACTTGAAACCTGGTCTCGTTGGCAATAA CTCGTTGGCGTGCAGGACGCCGCAACCGTACTTCGGCATCACCGCGTCCGACCTGAATTGGCAGCAAGCGCGCT GCTGGCCGGCATGGTCAATCGACCAGCACGCTCAACCCGTACACCAACCCGACGGCGCGCTGGCCCGGGAACGT GGTCTCGACACCATGATCGAGAACCTCCCGGGAGGCAGGGCTTGCCTGCCGCAAGGCCGATCCGCTGGGGT ACTGCCGAGCCAATGAGTTGCCCGCGGCTGCATCGGGCCGGCACCG

Clone Rv66

:::::::Rv66SP6.seq:::::::  
 ATACTCAAGCTTGATAAAAGATCGGTGAGCGCATICGATTGCTCCGCCGGTTTGCCGCTGCGCCGGCGAGCTGC CGT GACCGTCTATTGGGTGATCAGATACTGGGCTAGTCGGTGGGGTGATCGAAGATCGCGTGGCCGGCA GCGTTACTGCGGTGACGGCTGTTAAGCGGTTACGTACCTCCACGGCACTCAAGGAATTAAATCCGAAATCGGAAACCG CCTGGCCAGCGTCAATCCGGCAGCGCCGTCGCGCCCAAGCACCGCTGCGCATGCTCACATACCACCTCCATCGTG CGCGAATTGCTCGTCCGACCGACCCGGCAGCCGGCGAACCGGAAGA

:::::::Rv66T7.seq:::::::  
 CCTCATCATATGCCGATAGAGCTCTACATATTCAAGGAGATCACCATGGCTCGTGCAGGATCGACTCGGGACCAC CAACTCCGTCGTCGTTCTGGAANGTGGCAGCCNGGTCGTCGTCGCCAACTCCGGAGGGCTCCAGGACCACCGTC AATTGTCGCTCGGTCGCCCCGCAACGGTGAGGTGCTGGTCNGCCAGGGCCAAAGAACAGGCAGTGACCAACGTCGATCGC ACCGTGCGCTCGGTCAGCGGACCATGGCAGCGACTGGTCCATAGAGATTGACGCAAGGAATACACGCCGGAGATCT CGCCGCAATTCTGATGAACTGAACCGGACCCGAGGGCTACTCGGTGANGACATNACGACCGTTATCACACCCCGCTNC TTCAATGACCCACGTCNGGACCAAGGACCCGGCAATCGGGCTACTTNGCGATNGTCNACAACCAACGCGNCGC CTGGCTACGGGCTCAACAAGGACANAAGACACAATCCGCTCGATTGGTG

Clone Rv67

:::::::Rv67SP6.seq:::::::  
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:::::::Rv67T7.seq:::::::  
 TGGCCGGGCTGGTAGGCCCGTATGGCAAGGTTCCGCTCAATGTGGTGATGCAGCAGGACTACGTTGCCCTCAAT CAGCTCAAACGTCACCCCGTGGCGAGCCCTATTGGCCGTTGCGGATCGGGTGTGCGCAGCGTGGCGAGCTGGCGAAGGCAACAGGT AAGAACCTGGTGGCATGGGTCGAGCCCTATTGGCCGTTGCGGATCGGGTGTGCGCAGCGCAGGAGTGGCGTCAATCCACCCGCTTCACCGATCTTTCGTCGAAATGGCGTGGGTATACGTCGCGATTCCACCGAGGCG CTCAACACCGCCCTCACCGATCTTTCGTCGAAATGGCGTGGGTATACGTCGCGATTCCACCGAGGCG GAATCCGCTGAGGCCGAGCTGATCCGGCTCGCCCGGGTGAATCCTGGCTGTGGTGGTTTCGAGCATAACGAGCAG ATGCGAAT

## Clone Rv68

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:::::::Rv68SP6.seq::::::::::
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GTCAGCCGATCCACTGGATGCCCTCTCGGNGTTCAATCANGTACANGCGACGTTGCCACCATCGTGCAGGGCAC
GGTAGCGAGAACCGCCGACTTCACCGATTGCCCTCGGTATGCCGTGAACAGATCGGGCTATTGTCGACAGCCAG
TGTGATNCGTATTGCCGCCGCTCCTCGTCAACGATGCCAACACAAATCCGGTGGGGACGATAGCGGCTGACAA
NGTGGGGCAACACAATCACATGCCACATTCACGCCAACACCAGACTTCGTCGATGNGCCG
```

```
:::::::Rv68T7.seq::::::::::
CACGCCGTCTGGCCGATCCGAAGATCCCTTGCCGGCGTGGCGGCTCTGCTCGCGGTGTTGTACACTTCTGAACA
CCTCGCACCGACACCACCGCTNGCTGAACACCGCCAACATCGGCAGCAGATCTTGATGGTCTGGTGAATCCA
CGGTGACTTTGGAGTGGAAAGGCCATACTGATGCCCGCCAGCACATGAGCTAGCGCAGGAAACACAGCAGCCGC
TCACCTTGCAGCAGCGTCNGGTATGCCCTGGGCCCTTAATCTCGTGAACAGTTGGATTGGTCAACTGGCAG
CCTTGGGTCTCCGGTGGTGGCANGTGTANATAAGCTCCGGTCCGTCAACGTANTGCGCAGGCCGGTTACTCGG
CGGGTCAACGAGCCCCGCTCGTGGCAGCNATCAGCCTTGGACCAGGGATTCAACTCCGAGGCCGGCTCCGAAA
TCGGCACATGTCCTTGATCGTCGCAACAN
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## Clone Rv69

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:::::::Rv69T7D3.seq::::::::::
GGCCATGTCACATCGGTGGTACAGGTAACCGCGCCGTGCGCGGTCTCGGAGATCAGAACGTGGTGCAGTTGAAC
CGCGGGCTTCAGCAGTCGCGATAATCGCGGAAGTCGGCGCTGCCGCCCAACTAGCGCAGTCGCCACCTAGCA
CACCGATGGCGAAGGCCATGNTCCGGCACGCCGCCGCGTGCATCACCAAGTCATCGACTAGGAAGCTAACCGACA
NCTTGTGCAGGTGTTGGCGAGTAGCTCGGAAAATCGGCTGGAAACCGCATCAAATGGTCGGTCAATCGAACCG
GTTACCGATCGTCACAAAATCTCCGTCCT
```

## Clone Rv6

```
:::::::Rv6SP6.seq::::::::::
GGGTCTACAACCACCGGGTCTGACTTCTGGGCTTCACCGCTCGCGCGTGCACAAACAGCGGGTGAACCGACA
CTCGTGTGATGTCAGCTACACCTCCGGTAGGGACCCAATCGACCCCTACCCGGCTATCTCACCCCCGATCTCCAG
GCTCCGCCATCGCAGCCGGATCCC
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```
:::::::Rv6T7.seq::::::::::
CAGGCATGCAAGCTTGTCTGATTCCGTGGCACTGTCAGACATATGCCCGCTCCTCATCGCTGCCTCGGCATCG
TCGCCGGCGGTCACTGGCGTACCCCTACCAAGCCGAACCGCAGAACGAGAACGTGTTCCATTATTAGGGTGTGAGCACC
AATACCAGATTGCTCAGCAGACTCACGCGACCCGGACGGATGTCAGCCACCACGCCATCTGGGTGGTAGCGG
GGAAAATACGGCTAACCGCGCTCCGGTGGCGCAGCCCAGCGCAGACCCCTCGCGGGACACGGCTAACACGACGAC
CCATAGTTGTTCTTGCCGGATGGCGTGTGACATATCGGGCGCCGGCGCCGCC
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## Clone Rv70

```
:::::::Rv70SP6D2.seq::::::::::
NCTACGCTGCTGAATGTTGCGCCGGAGGANCTCAAGACCCACGCCGTTGTACCGGACNTGCACATGTTCAACCG
CCGGA
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:::::::Rv70T7D3.seq::::::::::
CTAACCAACAAGCCATGGTGGTGGCGCGTGCAGAGGGTGGCGGTGCCAACACGGGAAGATGCCCTGAGCGTCG
TCGACCGCCGCTCGAGTTGGGTATAACGAAGTACTGATGCCGATCATGTCGACGTGTCGTCATCAGCGTCAG
CGCGACCCCTCGACGAGCCCTCGGTGCCCGCGCCAGGGCACCAGCTGTTTAGGCCATTGTCGTCGCCGGTAAT
AAAGGANGTCGGTCGCCCTCCGCTGCTGTGGTTGCCGAATAACATCTCCCTCTGCAACAGGATGAGAATGGTTTA
ATTGCTC
```

## Clone Rv71

```
:::::::Rv71SP6.seq::::::::::
CTAACGCTTCCGGTCCGCCACTAGTACCGCGTTGCCGGCCCGACCTAGAATGTTCCGCCATTGCCGTTTC
CTCCGCCGCCGGTT
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## Clone Rv7

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:::::::::::::Rv7SP6.seq::::::::::::
ATACTCAAGCTTATCTAGGCGCAGCTGATTGGTCTGGGTGCATTGCCAGCTGCGCGAGCCTGGCTCACTTCAACT
ACAACAACCGCAAACAATTGCCGCCCTCGGATCCGAGTTGGTACGCCAATGANCACCATTCTCGGTGA
ATCAGACTATTCTGAGTACTTGATCATCCACTCTGACACGACCTGCAACCCCGCGCCCTGCGACCTGGAGC
AGCTGGCGAACGTGTGAGCCANATCCCAGGGCGTTGCCATGGTTCGCGGTGTGACCCGGCAAACGGGAAACCGCTG
AACAGGCCGGCGACATACCAAGGCCAAGTTGCCAAGCGGTGGCGCGTCGCAATGATCGATGAGCGCA
CCGGCGACCTGAATCGGCTGGCATGGGTGCCAACCTGGCCGACAATCTGGTGGCGTCAAGTCAGGCC
GGCGTTGGGTGTCCGAGCCTGTGCTTACTCCA
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## :::::::::Rv7T7.seq::::::::::::

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CAGGCATGCAAGCTTTTGAGCGTCGGCGGGGAGCTTCGCCGCAATTCTACTAGCGAGAAGTCTGGCCCAGTACG
GATCTGACCGAAGTCGTCGGTGCAGCCACCCCTCATTGGCGATGGCGCCACGATGGCGCTGGGACCGATCTGTG
CCGCTTGCACGGCGACGGGTAGGTGGTCAAGTCCGGTCTACGCTTGGGCTTGGGACGGTCCCACGCTGGT
GGGTTGCGCCGCAAAGCGGGGTGGGTGCCATAGGAATGCCACCCGCCGGCACTGCACGGCAAGTCCCCG
CGCGATTCAGGCATCGGGACATCATGCTCGCTTACTCCTCGACCAGTCGGCGAACAGCTCGATTCCCAG
CCCACGCATGGTG
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## Clone Rv80

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:::::::::::::Rv80SP6.seq::::::::::::
AACAGCTATGACCATGATTACGCCAAGCTATTAGGTGACACTATAGAATACTCAAGCTTGTAGAAAAAGATCGGTGA
GCGCATCGATTGCTCCGCCGGTTGCCCTGCGGGCGAGCTGCCGTACCGTCTATTGGGTGATCAGATACT
GGGCTAGTCGGTCGGGTGGGTGATCGAAAGATCGGGTGGCCGGCAGCGTTACTGCCGTGACAGCTGTTAACGGT
TACGTATCTCCACGGCACTCAAGGAATTAAATCCGAATCGGAAACGCCCTGCCAGCGTCNAGTCCGGCAGGCCGT
CNCGCCAGCACCGCTGCCATGCTCACATACCACCTCGATCGTCGGGANTTGTCTCNGCCGACCGACCGG
CCANCGGGCGGAAACCCNGAAGACCCAAGAATTCATCACCACCATCGCTAGC
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## :::::::::Rv80T7.seq::::::::::::

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CCTTCTGACACCCACCTGCCATCGACCTTGAGCAGTCCGCTAGTTGGTAACATGTGACCGCGATGGCGGG
TGAACCGTACTGGGTGTCGGTGCAGCTCATCTCACACGCCGTAGCGCAGCGCTCTCGATCTCCGACTTAA
GCGAACCCGAGCCCGTGGAACACGAAACATCNAACGGCTTGGCGTCNGCCGGCAGTCCGAGCTTGGCGCCACCT
GTTGCCCTGCGCAAGGATGTCNGGGGAANCTTGACGTTGCCGGCTTGTANACGCCATGCACGTTGCCAACGTCN
CGGCCAGCANGTATTGCGTGTCAACCGCGCCANCGCCCTCGATGGTTTCTCGAAGTCCCTCCGGCTGGTACA
GCTTCTCGTTGATCTCGTTCGCCACGCCGCTCTTCGCCGCCGACG
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## Clone Rv81

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:::::::::::::Rv81SP6.seq::::::::::::
AACAGCTATGACCATGATTACGCCAAGCTATTAGGTGACACTATAGAATACTCAAGCTTGGAAAGGAGATCCCCGGG
AACCTGGTGGCAACCCGCCATTGGGTTGTTGGGATTGCCATCGCGTGAANGAAAGCTCGTCTGGAGACAGCGGG
TCGGCGAAGCCGAAGATTGCCATCACTAGTGACGANATCGCGCTCTCGAGTANCCNAAGACAGTGACGTTG
TTNCCGGCGCAATTGCTGCCAATCGCAGTTGCCAGAATGACNGCACCTGCCACCGGANGAATCNAAGTGAGG
TTCTTGATCACGACCAACCGGTNGAGCCTTGGGCGTGAAGANCCTGCGCNATAACACCCGGACGCTGCCACTC
ATGTCAGCGCTCGCGANCTCNACATATCT
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## :::::::::Rv81T7.seq::::::::::::

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TCCTGGTATCGANGGCCGGTCCGCCGAAAATCCGGTTGGGTCGGGTCGCGGTTCCAACCTGANCGGGTCC
GCAGCTGATTACCGTGGCAACGCCGGCACTCGCATAATGCCACCCCTCACCCGCCCGCCGATCA
CCCCAACCTGATCCAACGACAACCGCCCTCCGCATACCCGGCGCAGCGGGAAACTCCGGCAACCGCCGCC
CCGTGGCGATCGTGTGGGCGTTGCCATGCCAGAACANCCATCTTCCAGGCCACCAACCCGCCACCGCGCCCCCG
TCACACCCCACAACCGTCGCGATCCAGCTGCCACGATCTCCACAATGCCCATCAATCGCATTGCGCTGAACGG
GCAACTCCGCCAACTCCCTCAA
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## Clone Rv82

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:::::::::::::Rv82SP6.seq::::::::::::
AACAGCTATGACCATGATTACGCCAAGCTATTAGGTGACACTATAGAATACTCAAGATCTGGTACCCATCCGTGATA
CATTGAGGCTGTTCCCTGGGGTGTACCTCCACGAGCAAACACGTAAGCCCTTCAGAGCCAGATCCTGAGCAAG
ATGAACAGAAACTGAGGTTTGTAAACGCCACCTTATGGCAGCAACCCGATCACCGTGGAAATACGTCTCAGC
ACGTCGCAATCGCGTACCAAACACATCACCGCATATGATTAATTGTTCAATTGTATAACCAACACGTTGCTAACCCG
```

TCCTCGAATTTCCATATCCGGTGCCTAGTCGCCCTGCTTCTCGCATCTGTAGGCCTGAGAAGAAACCCAAAC  
TAAATCCGCTGCTTACCTATTCTCCAGCGCCGGTTATTTCCCTCGCTTCCGGCTGTACATTAAACTGTGCAA

## Clone Rv83

:::::::Rv83SP6.seq:::::::  
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GAACCTCACGGCGTGGATNAAGGTACCGGCCGGATTTGCGCAATGGCAGGTTGTCGCCGGCTTGANGTCCCGT  
AGCGCCGGATTCCACCATCCCCTGCGAAANTCCGGTGGGTNCATGATGTNNCGCTCTCCCCCNANATAATG  
GANCAACGCNATCCGTGCCTGACGGTTCGGGTNTACTCCATGTNCGCACCTTGGCGTGANACCATTTGTCTT  
GCGGCGAAAGTCNATCATCCGGTNAAGCNCNTATGANCGCCGCTTGTGCCGGTGGTAATCCGCCATGCGCTT  
GCGTCCACCGCGAACGTGCAACGGGGCNCCAAGANTTCTCCNGGGTGAACCGGTNATCT

:::::::Rv83T7.seq:::::::  
TGTGTGTGGTGGTAACCCATCTGAGCAGTGTGCCAACCGGGGAGCCAGCTCCAATTGACGTGAGCCCCTCACTT  
GCTGGGTAAAGCGTCG

## Clone Rv84

:::::::Rv84SP6.seq:::::::  
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CAACGGCACCGTGTGGATCNGGTCTACCGCACACATNGACTGGAGCTTCGGCGAANTCATCGCTATGCCTCGCG  
GGGGGTGACGCTGANCCCNNGGTGACNTGTTGTCNGCTCNGCACGGTGCCTGCACGCTCNTCNAACACCTCANGCC  
ACCGGAATCATTCCCNNGCTGGCTGCACGANAGCGANNTTGTNCCCCTCCAAGTCTAAAGGCTGGCGANANAAGCAN  
AACGTCCCAGCNAACGGCACTCCTTTCCNTTGCTCTT

:::::::Rv84T7.seq:::::::  
GAAATCATTGATGGTTTGGTCAAGCCTTCGCCGAGCCAAATTCCAATCAAGAGGCCAAGGCCGT  
ACCAATCAGCCCGCAACGAGGGATTCCGTATTACAGCCAAAATAACTGCTCTGGTTACACCCAAACAGCGCAA  
TATGGCGAAAACGGTGCCTGACGACATTTAAATGTCACGGTATTGAGATTAAAAGATACCCACCAACAANGC  
AATCAAACGTGAGAGCGGTTAAATTGACCGTAAAGCGTCCGTATCTGTTGACNGTGTCCGTTGGTATCCGACGT  
TTCCATACGCACACCGGCCGGCAGTCTTGATGCGTNTTGAATGGCCTCATCTTGATGATCAAATCGATGTN  
GCTCAGTCTCCGGCATATGGAACAACCTTGGCGTGGAAATATCAGCAATGATA

## Clone Rv85

:::::::Rv85SP6.seq:::::::  
CTTTCGCCCAGGCCGGCGCGGATGTCCTCATCGCTTACGAACATCATCCGAGCTTGACGCTGTCGCCAACAGATCC  
GCGCTGCCGCCGCCGCCACACCGTGTGGCGCATCTGGCCCATCCGAGGTGACCGCGCAGCTGGCTGGTCAGG  
CCGTCGGAGCTTCGGGAAGCTCGACATCGTGTCAACACGTGGCGCACCATGCCAACACGCTGCTAACGACCT  
CGACCAANGACCTCGCGACGCCCTCGCCTCAACGTGGCACCGCCACGCGCTGACCGTCGCGGGTGCCTGA  
TGCTGGAACACTCCGGCGGCCGGCAGCGTGTACACATCAGCTCACCAGGGCGCTGGCGCGGGTTTC

:::::::Rv85T7.seq:::::::  
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AGGGGGAAATCANCCTTGTGTCGAGGCTGATTCGCCGGATCACCGTGGAGCGCGCAACAAAGTTCATGGACT  
GGTGGCATCGAAACGGCGTGAACCGGCTTCNTCGCTCAGGGTGCCAAAGACAACCTTGATCGCANGGAAGCGACG  
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## Clone Rv86

:::::::Rv86SP6.seq:::::::  
GAGCTGGCCGAGCTGGACCGGTTACCGCGGAACCTACCGTTCTCGCTCGACGACTTTCAGCAGCAGCTTGCGAGCG  
CTGGAACCGGCCACGGTGTGGTGTGGCGCCGACCGGGCTGGCAAGACAGTGGTGGCGAGTTGCCGTGCA  
CTGGCGCTGGCGCCGGCAGTAAATGTTCTACACCCACGCCGCTGAAAGCCCTGAGCAACCAAAGCACACC  
ACAGCACGCTACGGCGTGAACAGATCTGGCTGCTGACCGGTGACCTGTCACGGCAACGCCGGTGGTGGTGA  
TGACCAACCGAAATGCTGCGAACATGCTAC

Clone Rv94

:::::::::::::Rv945P6.seq:::::::::::::  
TCCTTCTCGGTATCGGTTGGCTGTCACCANCAAGTGGTAGTTCTTCACGTNCTGTTGTCAGCGTCNAGCCGTC  
CGCGTGTNANGTCNCGGACCGTATCCCGCCAGGCCGGTCANGGTGCCCTTCCANTCCACGCCGCTGTGGTCGGC  
AACGCTNATCTTCAATCGAGACCATGCCAGCTTCATCNTGTTGGCATCTGTCNNACGGCACCTCNAACCGGCCT  
NCTAGTACNCCACNCNATCNTGTTNCCTCNCGTNACATCCTCGATNCCNCNTGCACTTCCCTCGANCNCCTGGC  
CGAGGCCGGTGGCANTNACCTCNGAGCCCCATTGGACATCANCCANCCCGCCTGCGAACGGGAACGTCAGCNCNTGG  
CGACAACCGGCCAACAN

:::::::Rv94T7.seq:::::::  
CACNCCTGATCGCNAGCCCCGTAGAAATNGTTAGCCAGTTGGTGCAGCGCTCGTGCCTGGCGTNATCTCGTCGA  
GCTCNTCTTCCATCGCCGCGGTGAAGTCGTAACCGACNAGCCGACCNAATGCTGCTCNAGCAGACCGGTTACNNNA  
ACNCCNCCTCCTGACNGCACCAGTGCNCNTGCCCTTCTTGTGCACGTACCCGCNATCCTGGATGGTCTTGATGATCNA  
TANTNTGTCGACGGGGCCGATGCCATCTCCTCNAGCGCTTGACCAGCGACNCCTGGTGTATCGGGCCGGCGGG  
TTNGTGGCATGGCCGTCTGGGGTCACTCNACNATNTTCAACCGTTGACCCGGGGTACA

Clone Rv95

:::::::::::::Rv95SP6.seq:::::::::::::  
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GCAAGGGTNGCCTNATTCTCTCTGGCATGGTNCCACACCGGAATGNCGGTAAGTCTGGTCGGCACCTGGCC  
GCTGCGGGTTGGGTTGGGATTGCTCGCTCGGTANTAAAGGTGCTCGCTGGTGTNACNACTAATCNCNATATACNCTTANC  
GGGAGTNGNCGTCCCGATCCTNGCCCTGCCGCNGGATCNCGGTGCANACCGCCACCGGAACTCNCNAAAGTGC  
TCATCGGGCTACCGGCCATCTCCCCGGATTCTTCGCGGCNGTNCCGGGACCCGGACTGTGACNGGCCAA  
CGGCTCATCATCG

:::::::::::::Rv95T7.seq:::::::::::::  
CCGGATAGCGGTGCTGAACCTCGCCCGTCCCTCCANCGCATTGAGCTTCAGCCCGACCGGCAGGTNNGGAGTCGGC  
ATGCGGTCTTCGCCCCGACCCCGCTGGCTAAATANCCACCCCCGAGCGCGGTACGGTCTTGACCGGGACGACGC  
ATACCGGCAGCGCAACATCNCCGCGGGCTGCAGCNTGAACGTTCAATACCANTCNAACAGTGTCCGCGCGTNAAAAC  
CCGANCCGGCGGTGGCTTCNGTAATCAACGGCTCTGCGAACCGAGCTGCAAGTCGCCGGTGCACCGGCGTTGACGA  
TCTTGATGTCTGCGANCTCGCGCACCGAGCTGACGGCCCGGGCA

Clone Rv96

:::::::::::::Rv96SP6.seq:::::::::::::  
CCTCCCGACCACATACAGGCAAAGTAATGGCATTACCGCGAGCCATTACTCCTACGCGCGAATTAAACGAATCCACCA  
TCGGGGCAGCTGGTGTGATAACGAAGTATCTCAACCGGTTGAGTATTGAGCGTATGTTTGAATAACAGGGCGCAC  
GCTTCATTATCTAACTCCCAGCGTGGTTAACAGACGATCGAAAATTCTATTGCAGACAGGGTCCCAAATAGAAAG  
AGCATTCTCCAGGCACCAGTGAAGAGCGTTGATCAATGGCTGTTCAAAAACAGTTCTCATCCGGATCTGACCTTT  
ACCAACTTCATCCGTTTACGTACAACATTAGAACCATGCTCCCCAGGCATCCGAATTGCTCCTCCATCCA  
CGGGGACTGAGAGGCCATTACTATTGCTGTATTGGTAAGCAAATACGT

Clone Rv9

:::::::::::::Rv9SP6.seq:::::::::::::  
CTTCACNTCCGTACGGCTCGGGTACGCTCGGTNCATTGTGCGAGTGTAGATGACGACCGGGACCTCGTCGGCATC  
TTCCATAGCCCGCCACACCTTCAGTTGCTCACCGGAATCCAACCGGTANAAGGTCGGCGANCCTCNGCATTGGTCATC  
CGGGATATGCCGCTCGGGACGGTCAANAGCCCTCGGTCCGGCOAGCACTCCGCAGGCTCGTCGGGTGGTCGGCAGC  
CGCATGGGCCACCATCGCATTCAACCAGGTCTGCGCGAATCACCAGCACGTANACGGTTCCTTCTTAAGCAACACCGA  
ANTTTCAAGGACCCGAATGCTCCGGAAACATGTACCGTAGGTCGGTATTCCGGTACCGGCTGANCATTGAGCACGC  
CGGCCAGCACCGCACGAACCAGGCAATCAGCCGCCCGCACCCGACCGCGG

:::::::::::::Rv9T7.seq:::::::::::::  
CAGGCATGCAAGCTTGTGCCGCCAAACCGAGCGTGAGCACGCCGCCAGCCACCACGCCGGGTGGGCGCCGGGC  
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GCGGAGCTACATCGGCTCGGCCGCCAGTGTTCGGGCCCTTTGCGAGGTCGAGGTCGATACCGATTGCGCATCCGC  
AGCCGACCCCTGGACGACAGAACCGTGCCTACGAATTGCTTGTCCGGCGGGCCAAAGAACAGCTTGGCATCCTGGC  
GCGATTGGCCGGCGCGCTGGTCGCCAAGGAAGACCCGTTCCGGTGTGAT

**Table 4 :** End-sequences of the polynucleotide inserts cloned in the named recombinant BAC vectors contained in the I-XXXX *M. bovis* strain Pasteur genomic DNA library.

RvXXXSP6 corresponds to the SP6 end-sequence of the clone RvXXX.

RvXXXT7 corresponds to the T7 end-sequence of the clone RvXXX.

RvXXXIS 1081 corresponds to a region located close to a copy of the IS1081 repetitive sequence (Insertion element).

The character « - » denotes an uncertain base residue.

Clone X0001

:::::::::::::X0001SP6.seq:::::::::::::

AAG-  
TCGGGTTTCCACACGCGCGTTGACCTAGTCATATGTAATCATGTGTAACCATGTCGGGGCGCTTTCGACGGCCG  
CGAACCCACCGA-ATTCCTGTGATTCACTGCATGCGTACCATCTGGCACAATTGAGCA-TTGTCT-  
TCGCGGTGGTCGG-CGGGTTGCGTGCCGCTGCGA-ATGCACCA-  
TAAGCCCGAACCCACCGGCTTGGTGACCACCGCACGCTGCGTGTGGGGGTAACCACCTCCGCGACCCCAAGGATGGT  
CATTCCAATGAACCGCTGGACTTCGTCCA-A

:::::::::::::X0001T7.seq:::::::::::::

GTCGCGGTTCGATCGACCGATCTTCACCTCGTAACCTCGATGCTTAGCAGGATCCAGCTTGACCGCGTTGGCTCT  
ACCCACTCTTGAGTGGCGCGTGCCTGTGCCCCATCGGTGTTCATGACGAACGCTCGAAAGACTTCTCTTGTG  
AGCCGAATGTCGCTAAAGAAGTTCATGTCGGGAAGTAGACCCGGTCGCCCTCACGTGGTACTCCTTCGAGG  
TCCGCTCTCGCCGGATCCGATAAAACACCGGCCCCAGGCACCGCAGCGTAGTTCGAACGGCTCAGGTAGGTGTT  
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TCGAAGATGCCCTCTGGAGGGCGCGA

Clone X0002

:::::::::::::X0002SP6.seq:::::::::::::

AACTCAAGTTTACGGTATCGCGCATCACCTGGTTCATGAACTGGAAGCAGCGCAGCGTTCTTTCGGCCGCA  
ACATGAGCCAGCCTCTCGTCGGCGGTGGTGCAGGTGCTGGCAGCTGGCGACAGCCGCTGACCGCTGAAA  
CCAGCTTCCATATCCCGCAG-  
AACGACGCCAGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGCGTTCTCCACCGACCGGGGGGG  
TGT

:::::::::::::X0002T7.seq:::::::::::::

GTGCAGGTTCGACAATGGTGCCGGTTCGGCGCTACGTGCCATCGAGACACTGGCGCA-GCTATCGCACCCGTT  
ATCGGCTGCGAGCAAATCGGGTATGCGTTCTGAGCATGAGTCGGCGACCGTGTGACACCCACGACGG  
AAAGACGAGATGCCGTCAGCATGTTGCCGGATTATCAGGACTGACCTCTGGTGACCCGATGTTGGTC  
GCGATGCGTGGCGCCGGCGGTGGTGTGGCTGGATAGCGAGGTAGCGAATTCTCGTGGCAGCTCGAA  
AGGGCCTGCCGGTGGCGGT

Clone X0003

:::::::::::::X0003SP6.seq:::::::::::::

TTCGAGTCATGCGCCCGCCTCGACCAAGAA-ATGCACGTCG-  
GGTTCGATCGACCCGATCTCACCTCGTAACCTCGATGCTTAGCAGGATCCAGCTTGACCGCGTTGGCTCTACCCA  
CTCTTGAGTGGCGCCGTCGCCTGTGCCCCATCGGTGTTCATGACGAACGCTCGAAAGACTTCTCTTGTGAGCCG  
GAATGTCGCTAAAGAAGTTCATGTCGGGAAGTAGACCCGGTCGCCCTCACGTGGTACTCCTTCGAGGTCCGC  
TTCTC

:::::::::::::X0003T7.seq:::::::::::::  
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 CCGTCTGGCACAATTGAGCAGTTGTCGCGGTGTCGGCCGGGTTGCGTGCCTGCGAGATGCACCAAT  
 AAGCCCGAACCCACCGGTTGGTACCACCGCACGCTGCGTGTGGGGGGTAACCACGCCGACCCCAAGGATGGTC  
 ATTCCAATGAACCGGCTGGACTTC-TCAACAA

Clone X0004

:::::::::::::X0004T7.seq:::::::::::::  
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 CTCTTCGGTGACCTGCCGCCGCCAGCTGGCCAGTGCCTGGCGTGGCCGCCGCGACGATCTGGCGT  
 CCACGGTGGTCGGGG

Clone X0006

:::::::::::::X0006T7.seq:::::::::::::  
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 CACAGCGATTGACCCAGCGCGCGCGCGCTTGCCGAGGGCGAACGAAGCGGTGCCAACCGCAATCTGGTCAG  
 CTCCATCATGCCGGTGAGTCCCTGCCG

Clone X0007

:::::::::::::X0007SP6.seq:::::::::::::  
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 GGCGCTCCGGCGACCCGACCATTCGTCGCCGCTAACGCCATCACGGATGACGCGCAGTCGCTGTCTA  
 GCTCCACCATGCCCTGCACACCGCGGCCAG-ACCCATTGGCGCTCGCACTCGTA-  
 AGCAGGTAATCCTCGTCGACGGACTCGTAACCACGCCAGCTCCGCTGCCAGGTGGCGGGGTTGACACCGGC  
 GGGCATCGGGATGGACGACGACGCCGTGCTGACGGCCCTGTC

:::::::::::::X0007T7.seq:::::::::::::

AGCGGTTTCCCA-  
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 CTTGAGCCGGTGCAACTCGTCCGGCCGGACGGTACGCCGACGGCGAACGCCGCTACCCACCGTGACCTCCTGAGGA  
 AACGCTGCGTTGGCTTACGAGATGATGGTGGTACCCCGAGCTGGATACCGAATTGTCATCTGCACG

Clone X0008

:::::::::::::X0008SP6.seq:::::::::::::  
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 CGCCGCCAACGATCTGGCGTCCACGGTGGTGGTCATGCCCGAGCAGGATGGCGAGCGGCCGGTCAGCC  
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 GCAACCTCGGGGGTGGCGCC

:::::::::::::X0008T7.seq:::::::::::::

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 AGCGCAGACCCGACGATTCCGTACACCGCCACGCCGATCAGGCCCTGGGCCAGCTGGCTATATGGCGCGATGGT  
 ACGATGGCCAGCGCCACATACATTGTGGCGGCCAGAACACCGCGTGGGGCGGCGTCACTGAACACTAGGCCACG  
 CAGATGCCCGGGTCAACAGGTTGACCATCAGAAAGCCTGCGA

Clone X0009

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 TCTGACGCGTAACCGCGTTGTGATCGCGAGCTGAGGAGACGGTATGGGGAGGGTCTCGGAGGCCATCTGGGATGT  
 TGATGTCTGCGATCTTGAGCCGGTGCACACTCGTCGCCGGACGGTACGCCGACGCCAACGCCGCTACCCCGT  
 GACCTCTGAGGAAACGCTGCGTTGGCTTACGATATGATGGTGGTACCCG

:::::::::::::X0009T7.seq:::::::::::::  
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 GTCGACGGACTCGTAACCACCGCCAGCTCCGCTGCCAGGTGCGGGGTTGACACCGGCCATCGGATGG  
 ACGACGACGCGGTGCTGACGGCGCTGCGCACGCTGAGCTGGACACAGCTAGTAAATGTAGCCTAACCTACTTA  
 ATGGGTCGAGCCCCCGGGGCGTCGATGTCAAACGTTGCTGACTGGAAGAAAATGCTCGTCGGGAGCAAATG  
 GCACC

Clone X0010

:::::::::::::X0010SP6.seq:::::::::::::  
 AATACTCAATCTTGTATCGGTTCCAGCAACAGCGATCGACGGCTCGCCCAGGGCGCTCCGGCGACCCGACCA  
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 CGGCCAGGACCCATTGGCGCTCGCACTCGTAGAGCAGGTAACTCTGTCGACGGACTCGGTAAACCACGCCAGC  
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 GACTCTGAGCTCG

:::::::::::::X0010T7.seq:::::::::::::  
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 GAGCCGGTGCAACTCGTCGGCCGGACGGTACGCCGACGCCGAAACGCCGCTACCACCGTACCTTCTGAGGAAAC  
 GCTGCGTTGGCTCTACGAGATGATGGTGGTCACCCCGCAGCTGGATACCGAATTGTCATCTGAGCGCCAGGGG  
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 CTGGTTGTTCCCC

Clone X0012

:::::::::::::X0012SP6.seq:::::::::::::  
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 GAGGCCGGCTGGAC-  
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 CTGCA

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 TTGAGCATGAGTCGGCGACCGCTGTCATGGTCGACACCCACGACGGAAAGACGCAGATGCCGTCAAGCATGTC  
 CGCGGATTATCAGGACTGACCTCCTGGCTGACCGGATGTTGGTGCAGTGCCTG

Clone X00013

:::::::::::::X0013T7.seq:::::::::::::  
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 CGAACCCCGGATGCTGCTGGTCCATTTCCTCGTGCAGCTGCCGCTCACCGGAACTCACTGGGCTGTGATACCA  
 GCAACTGCCGGACATGCGTGGTGGAGGTCGACGGCGTGCCTGAAATCCTGCACGATGCTGCCGTATGGCCTCC  
 GGGC

Clone X0014

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 TCCGATGCTGGAAGCCTACACTGCCCTGGTGCCTGGCC-C-GCGACCGAGCGCTGCAACTGGCGC-  
 TTGGTGACCGCAATACCTACCGCACCCC-ACCCGCTGG-CAA-  
 ATCATCACACGCTCGACTGGTAGCGCCGGTCGA-CGATCCTCGGCATTGGAACCGGTTGGTT-

Clone X0015

:::::::::::::X0015SP6.seq:::::::::::::  
 ACGCGCGCCGATCATATCTGCTATGGATGTACAATTCACTTCTGCTGTTATACCAACTGCCATGTTGGGACGCCCG-CC-  
 CTATGCTGACGTGTGAGATGCCGAACTGGCCCTGGCTCGACTGCCGGCTCTGGCTGATCCGACGCCGCTGG  
 ATTCTGGTGGCGTTGCTGGATGGCGTTGCTATCCGGCCAGCTAGCTGCCACCTCGGGTTGACCCGATGAAATGT  
 GTCCAACCATCTGCGTGTGTTGCCGGCTGCCGGTGGTA-TCCCAACCTATGAGGGCCGGCAGGTTGGTAT

:::::::::::::X0015T7.seq:::::::::::::  
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 GGCACCGACGCCACGACACACCGCCGTCGCCAACGCCACTGCATCGGTCGACGGCATTGGATGCCGG  
 TGCCCAGGCGCTGGAACTGGCTGGCTGGCTCGATGACATCGAATACGTGACACTGTATTGCTGCTTCCCTCG  
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 ACCTTCGCCGGCGGCCGTGGAGCAATTACGTACGCACACTCAT

Clone X0016

:::::::::::::X0016SP6.seq:::::::::::::  
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 TAAATGAGCAGACCCGTGCCGCAACGATGGTGGCGATCATCGGCCCCGAAACGATGGCCGGTC-  
 ATGCGCAACTTCTTCAGCAGCGCGGAAGGACGGCA-CCACCAGCGAC-ACCACACCACGAT

:::::::::::::X0016T7.seq:::::::::::::

GCGAA-  
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 GAGCTGGACCGCCCGCAGGTCTTGATTCAAGCGCAGGTGCTGCCAGCCACGGTGCCAACCGCGGCCCTGCG  
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Clone X0017

:::::::::::::X0017SP6.seq:::::::::::::  
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 CCGTATTCTCCGGCGGCCGGCTAACCCATCCCA-GCCGAACGGTTGGCTC-  
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:::::::::::::X0017T7.seq:::::::::::::

TGGTGGAGGTCCCCACCAA-ACCCGGCCGTAACCTGCTCACGGAAATGCGG-  
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 GTGGAAGGTGCCGTCGCGCAAGATCCGGCTGCTCACCAACCGTGCACGGCGCCGAAATCGTAAGCGCGGTCT  
 TGATGATGTTCGCTGCCGTCCTCGGTGGCGACGCTGCGTA-  
 TTGGCGACCGCCGGCCCCCTTGTGCGAAATCTCGCGACGACCTCATCGGCCATGCCAACCGGGCGCCCG

Clone X0018

:::::::::::::X0018SP6.seq:::::::::::::  
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 CACTCAAGGATCGCAAGGAAAGC-  
 TCAAGGATCGGTCGCGCCGCCAACGGCGCGTCAAGGAGGGATCGTCCCTGGTGGGGA-  
 CCTCCCTCATCCACCAGGCCGCAAGGCGCTGACCGAACTGC-TGCGTC-C-GACCGGTGACAA-  
 GTCTCGGTGTCCACGTGT-CTCGAAGCCCTGCCGCTCGTGTGATC-CC-CCAAC-  
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Clone X0018

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 GCCGGAATGGGATGTCCGG-ACGGCGAATCGCTA-  
 TTCGCTTGTCCCGTGAGGCCAGGTGGATGGGGGGAGGATC-TGGTGTCCGGGATGAT-  
 ATGGGCCGATGCCGCCGGTTGAAGTCCACTGGATCGGAATTGGGAATCGTGAATCCGACGTTAGGCCAAC

Clone X0019

:::::::::::::X0019SP6.seq:::::::::::::  
CTAACGGAATGAAAGCCCTGGTGGCCGT-  
TCGGCGGTGGCCGTCGCACTGCTCGGTGATCTCCGCCAAGCTGATCCGAGGGGGATCCGGCGCAGGTGA  
GGCCAACATGGTGGCCCCCAAGTTCCCCACGCTTGTGATCACACCGAATGGGCGCA-  
TGGGGAAATTCTGCCAGCCTCCGGGTCTACCCGTCCAAGTTGGGCGTACA-  
CCTCCCGCCGCTCGGGATGGCGCTGCCGACCCGGCTGGGCC-  
AGG\_ TCTCGCGCTGTACCGGAAGCCGACACTGCCGGC

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CCGGGGACAC-CCTC-  
ATGCTGCCGATGGACGCGTCGAACGCAAGCAGCTGATCGAGCTACAACGCCGCGGAAACGCTTCCGCCGCGGG  
CGTACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGGCATGCCACCGGAGCAGGCCAAGG  
GGCGTGCAGGTCGCCGGCGCACGGTGCAGACAAGGTGGTGTGGCGTCCGATCGGCCA-  
ACGACATCGTGGCGAAGATTCGCCGGTACGCCGATGATGTGGTGTGTTGGCAGGCCGGCGTTGT

Clone x0020

.....X0020T7.seq.....

CTCTGGGACCGGCCACGGTGCCTCCGGACGTGCTGGCCAGGTGTCGGCGGCCGCGTCATGGTGTCCCGGATCGGCCGCTGGCCAGAGCCCACCGGTGAATCTGGCGCTGGCCGACCACCGTGCCTGCTGGCGATCGTCGAGCGCTGGCGTGGCCAGAGCGAGATCCCGACGGATTGGGGCAGATGCGTGCCTCACCATCGGGGTATTGACGGCGTGCACCGCGGGCACGCCAACATCGCGCACCGCGTCAAAGGCGGC

Clone X0021

.....X0021SP6.seq.....

AATACTCAAGTTTCTGTCAGTCATTGCCAGCAGACCAAACAA-AGCATGGGACATACGGA-TCAACTACCCGGCAACGGTGAATTCTTGGCCGCGCTGACGGCGGAACGACGCCAGCGACCAC-TTCAGCAATGGCCA-CGCGTGCCGGGCCACGAGGTTGGTCTCGCGGCTACTCCCAGGGTGCGGCGTGATC-ACATC-TCACCGCCGACCACTGCCCCGCTCGGGTTACGCAGCGTTGCCGCCCCGAGCGGAC-ATCACATCGCCGCGATGCCCTGTCGGGAATCCCTC-GGCCGCGCTGGCGGGCTGATTAAAC

.....X0021T7.seq.....

TGCCGCGGATTTGGCTGGCTGCCCAATATTAGAATCGGGCTTCTTTGCGCGACAATAAGGTACAGTAAACC  
CTCGTTTGTGAGATGCGGGGGCGGGCGAA-  
TCGACCTCGAGTGAATGGATCTCGAGTGAATGGACAGGGCATGCCCTACGAGTCGCATCCCCATCCAACAGACCGGT  
GCTCTTGCACTGGACCCCTGAAGGTCCCGCACGGAGGGTGTGGTTGCCGGCGGGGTACGGTGCGGTAGCAGCTA  
GTGTTTGAACGAATTCTTGTGCTCCAACCTGTTGGTGTCAATCCAGTTCT

Clone X0175

.....X0175SP6.....

AA-CTTGC CGCT CGGCCGGGTC -AGCATCCAGCTGCTCGGCAAGGAGGCCAGCTAC-C-  
TCGCTCGTATGCCAGCGGTGAGATCCGCCGGGTC-  
ACGTCCGCTGCCCGCGACCGTCGGCGAAGTGGGCAATGCCGAGCAGGCAAACATCAACTGGGGCAAGGCCGGTCGG  
ATGCGGTGGAAGGGCAAGCGCCGTCGGTCCGGGGCGTGGTGT-AACCCGGTC-  
ACCACCCGCA CGGGGGTGGTGAGGGTAAACCTCCGGCGGCCGTACCCGGTTAGCCC GTGGGGCAA

.....X0175T7.....

A-TCGAAAGTGACCATCTCTACCTTGAGTGCCATACGCCGACCTATGCCCTGGATAGCTCGCGGAAAGAAACGCTTGCAGTGCGCGGAATAGGCGGCTACGTCGTGAGCGCCATCAACTCTCGCGCGAGTCATGCCAGCTGGCGGCGCCGACGTCGACCGTGGGATTCCGGTGC CGC GCG CGG GCAACGGCCGATCGTCGACCCGACCGCAGATCGGCGATCGGC GCGATGTTGTAACGCTGCATAGGCACTCCCGCGCTGGCAGGCCAGTGC GAA CGCCGCGCGGTGCGTCCG

**References :**

Altschul, S. F., W. Gish, W. Miller, E. W. Myers, and D. J. Lipman. 1990. Basic local alignment search tool. *J. Mol. Biol.* **215**:403-10.

5 Balasubramanian, V., M. S. Pavelka, Jr., S. S. Bardarov, J. Martin, T. R. Weisbrod, R. A. McAdam, B. R. Bloom, and W. R. Jacobs, Jr. 1996. Allelic exchange in *Mycobacterium tuberculosis* with long linear recombination substrates. *J. Bacteriol.* **178**:273-279.

Barany F., 1991, Proc. Natl. Acad. Sci. USA, **88**:189-193.

10 Bensimon, A., A. Simon, A. Chiffaudel, V. Croquette, F. Heslot, and D. Bensimon. 1994. Alignment and sensitive detection of DNA by a moving interface. *Science*. **265**:2096-2098.

Bergh, S., and S. T. Cole. 1994. MycDB: an integrated mycobacterial database. *Mol. Microbiol.* **12**:517-534.

15 Birnboim, H. C. and J. Doly. 1979. A rapid alkaline extraction procedure for screening recombinant plasmid DNA. *Nucleic Acids Res.* **7**:1513-1523.

Burg J.L. et al., 1996, Mol. and Cell. Probes, **10**:257-271.

Cai, L., J. F. Taylor, R. A. Wing, D. S. Gallagher, S. S. Woo, and S. K. Davis. 1995. Construction and characterization of a bovine bacterial artificial chromosome library. *Genomics*. **29**:413-425.

20 Canard, B., and S. T. Cole. 1989. Genome organization of the anaerobic pathogen *Clostridium perfringens*. *Proc. Natl. Acad. Sci. USA* **86**:6676-6680.

Chu B.C.F. et al., 1986, *Nucleic Acids Res.*, **14**:5591-5603.

Chuang S. et al., 1993. Global regulation of gene expression in *Escherichia coli*. *J. Bact.*, **175**(7) : 2026-2036.

25 Chuang, S., D. L. Daniels, and F. R. Blattner. 1993. Global regulation of gene expression in *Escherichia coli*. *J. Bacteriol.* **175**:2026-2036.

Cole, S.T., R. Brosch, K. Eiglmeier, T. Garnier, S. V. Gordon, C. Churcher, D. Harris, K. Badcock, D. Basham, D. Brown, T. Chillingworth, R. Connor, R. Davies, K. Devlin, T. Feltwell, S. Holroyd, S. Gentles, K. Jagels, J. McLean, S. Moule, L. Murphy, K. Oliver, J. Osborne, J. Parkhill, M. Quail, M-A. Rajandream, J. Rogers, S. Rutter, K. Seeger, J. Skelton, R. Squares, S. Squares, J. Sulston, K. Taylor, S. Whitehead and B.

30

G. Barrell. 1997. Genome Sequence of *Mycobacterium tuberculosis* H37Rv. *Microbial Comparative Genomics*, **2**:174.

Collins, D. M., and D. M. Stephens. 1991. Identification of an insertion sequence, IS1081, in *Mycobacterium bovis*. *FEMS Microbiol. Lett.* **67**:11-15.

5 Cousins D. et al., 1998, **36**(1) : 168-170.

De Wit D. et al., 1990, *J. Clin. Microbiol.*, **28** : 2437-2441.

Dear, S., and R. A. Staden. 1991. Sequence assembly and editing program for the efficient management of large projects. *Nucleic Acids Res.* **19**:3907-3911.

Duck P. et al., 1990, *Biotechniques*, **9**:142-147.

10 Guateli J.C. et al., 1990, *Proc. Natl. Acad. Sci. USA*, **87**:1874-1878.

Kievitis T. et al., 1991, *J. Virol. Methods*, **35**:273-286.

Kim, U. J., B. W. Birren, T. Slepak, V. Mancino, C. Boysen, H. L. Kang, M. I. Simon, and H. Shizuya. 1996. Construction and characterization of a human bacterial artificial chromosome library. *Genomics*. **34**:213-218.

15 Kwoh D.Y. et al., 1989, *Proc. Natl. Acad. Sci. USA*, **86**:1173-1177.

Landegren U. et al., 1988, *Science*, **241**:1077-1080.

Liu, Y. G., and R. F. Whittier. 1995. Thermal asymmetric interlaced PCR: automatable amplification and sequencing of insert end fragments from P1 and YAC clones for chromosome walking. *Genomics*. **25**:674-681.

20 Lizardi P.M. et al., 1988, *Bio/technology*, **6**:1197-1202.

Matthews J.A. et al., 1988, *Anal. Biochem.*, **169**:1-25.

Michalet, X., R. Ekong, F. Fougerousse, S. Rousseaux, C. Schurra, N. Hornigold, M. Vanslegtenhorst, J. Wolfe, S. Povey, J. S. Beckmann, and A. Bensimon. 1997. Dynamic molecular combing - stretching the whole human genome for high-resolution studies. *Science*. **277**:1518-1523.

25 Misumi, D. J., D. L. Nagle, S. H. McGrail, B. J. Dussault, Jr., J. S. Smutko, H. Chen, O. Charlat, G. M. Duyk, C. Ebeling, L. Baldini, G. A. Carlson, and K. J. Moore. 1997. The physical and genetic map surrounding the *Lyst* gene on mouse chromosome. *Genomics*. **40**:147-150.

Pavelka, M. S., Jr., and W. R. Jacobs, Jr. 1996. Biosynthesis of diaminopimelate, the precursor of lysine and a component of peptidoglycan, is an essential function of *Mycobacterium smegmatis*. *J. Bacteriol.* **178**:6496-6507.

Philipp, W. J., S. Nair, G. Guglielmi, M. Lagranderie, B. Gicquel, and S. T. Cole. 1996a. 5 Physical mapping of *Mycobacterium bovis* BCG pasteur reveals differences from the genome map of *Mycobacterium tuberculosis* H37Rv and from *M. bovis*. *Microbiology*. **142**:3135-3145.

Philipp, W. J., S. Poulet, K. Eglmeier, L. Pascopella, V. Balasubramanian, B. Heym, S. Bergh, B. R. Bloom, W. R. Jacobs, Jr., and S. T. Cole. 1996b. An integrated map of the 10 genome of the tubercle bacillus, *Mycobacterium tuberculosis* H37Rv, and comparison with *Mycobacterium leprae*. *Proc. Natl. Acad. Sci. USA*. **93**:3132-3137.

Poulet S. et al., 1995, *Arch. Microbiol.*, **163** : 87-95.

Ross BC, 1992, *J. Clin. Microbiol.*, **30** : 942-946.

Sambrook, J., E. F. Fritsch, and T. Maniatis. 1989. Molecular cloning: a laboratory 15 manual, 2nd ed. Cold Spring Harbor Laboratory, NY: Cold Spring Harbor. N. Y.

Sanchez-Pescador R., 1988, *J. Clin. Microbiol.*, **26**(10):1934-1938.

Segev D., 1992, in « Non-radioactive Labeling and Detection of Biomolecules ». Kessler C. Springer Verlag, Berlin, New-York, 197-205.

Sheng, Y., V. Mancino, and B. Birren. 1995. Transformation of *Escherichia coli* with 20 large DNA molecules by electroporation. *Nucleic Acids Res.* **23**:1990-1996.

Shinnick T.M. et al., 1987, *J. Bact.*, **169**(3) : 108-1088.

Shizuya, H., B. Birren, U. J. Kim, V. Mancino, T. Slepak, Y. Tachiiri, and M. Simon. 1992. Cloning and stable maintenance of 300-kilobase-pair fragments of human DNA in 25 *Escherichia coli* using an F-factor-based vector. *Proc. Natl. Acad. Sci. USA*. **89**:8794-8797.

Spargo C.A. et al., 1996, *Mol. and Cell. Probes*, **10**:247-256.

Stone B.B. et al., 1996, *Mol. and Cell. Probes*, **10**:359-370.

Trieselman B.A. et al., 1992. Transcriptionnally active regions in the genome of the archaebacterium *Haloferax volcanii*. *J. Bact.*, **174** : 30-34.

30 Trieselmann, B. A., and R. L. Charlebois. 1992. Transcriptionally active regions in the genome of the archaebacterium *Haloferax volcanii*. *J. Bacteriol.* **174**:30-34.

Urdea M.S. et al., 1991, Nucleic Acids Symp. Ser., **24**:197-200.

Urdea M.S., 1988, Nucleic Acids Research, **11**: 4937-4957.

Van Soolingen D., 1993, J. Clin. Microbiol., **31** : 1987-1995.

Willets, N., and R. Skurray. 1987. Structure and function of the F-factor and mechanism of conjugation. In *Escherichia coli and Salmonella Typhimurium: Cellular and Molecular Biology* (F.C. Neidhardt, Ed) Vol.2 pp1110-1133, Am. Soc. Microbiol., Washington, DC.

Woo, S. S., J. Jiang, B. S. Gill, A. H. Paterson, and R. A. Wing. 1994. Construction and characterization of a bacterial artificial chromosome library of *Sorghum bicolor*. Nucleic Acids Res **22**:4922-4931.

Zimmer, R., and A. M. V. Gibbins. 1997. Construction and characterization of a large-fragment chicken bacterial artificial chromosome library. Genomics. **42**:217-226.

CLAIMS

1. A method for isolating a polynucleotide of interest that is present in a genome of a first mycobacterium strain or that is expressed by said first mycobacterium strain and that is absent or altered in a genome of a second mycobacterium strain that is different from the first mycobacterium strain or that is not expressed in the second mycobacterium strain, said method comprising:
  - a) contacting under hybridizing conditions the genomic DNA of the first mycobacterium strain with the DNA of at least one clone that belongs to a bacterial artificial chromosome (BAC) genomic DNA library of the second mycobacterium strain ; and
  - b) isolating the polynucleotide of interest that fails to form a hybrid with the DNA of the second mycobacterium strain.
2. The method according to claim 1, wherein the BAC-based DNA library has been constructed from genomic DNA of *Mycobacterium tuberculosis*.
3. The method according to claim 2, wherein the BAC-based DNA library has been constructed from genomic DNA of *Mycobacterium tuberculosis* strain H37Rv.
4. The method according to claim 3, wherein the BAC-based DNA library has been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on November 19, 1997 under the accession number I-1945.
5. The method according to claim 1, wherein the BAC-based DNA library has been constructed from genomic DNA of *Mycobacterium bovis*.
6. The method according to claim 5, wherein the BAC-based DNA library has been constructed from the genomic DNA of *Mycobacterium bovis* BCG strain Pasteur.
7. The method according to claim 6, wherein the at least one BAC-based DNA library has been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on XX XX, 1998 under the accession number I-XXXX.
8. A method of isolating a polynucleotide of interest that is present in a genome of a first mycobacterium strain or that is expressed by the first mycobacterium strain and that is absent or altered in a genome of a second mycobacterium strain or that is not expressed by the second mycobacterium strain, said method comprising :

- a) providing at least one polynucleotide contained in a clone of a bacterial artificial chromosome (BAC) DNA library of the first mycobacterium strain;
- b) providing at least one genomic or cDNA polynucleotide from a second mycobacterium strain that is different from the first mycobacterium strain or at least one polynucleotide contained in a clone of a BAC DNA library prepared from the genome of the second mycobacterium strain;
- 5 c) contacting under hybridizing conditions the polynucleotide of step a) with the polynucleotide of step b); and
- d) isolating the polynucleotide of step a) that has not formed a hybrid complex with the polynucleotide of step b).

10 9. The method of claim 8, wherein the polynucleotide contained in a clone of a BAC DNA library of the first or second mycobacterium strain is prepared by

the following procedure :

- 15 1) digesting at least one recombinant BAC clone by an appropriate restriction endonuclease to yield a polynucleotide insert of interest; and
- 2) isolating the polynucleotide insert of interest.

10. A purified polynucleotide of interest that has been isolated according to the method of claim 8.

11. The purified polynucleotide of claim 10 which contains at least one  
20 Open Reading Frame (ORF).

12. The purified polynucleotide of claim 11, which is SEQ ID N0:1.

13. The purified polynucleotide of claim 11, wherein said polynucleotide is selected from the group consisting of :

- 25 a) a polynucleotide comprising at least 8 consecutive nucleotides of SEQ ID N0:1 ;
- b) a polynucleotide having a sequence fully complementary to SEQ ID N°:1 ; and
- c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).

14. The purified polynucleotide of claim 13, which is SEQ ID N0:2.

30 15. The purified polynucleotide of claim 13, which is SEQ ID N0:3.

16. The purified polynucleotide of claim 11, wherein the ORF encodes all or part of a polypeptide involved in the pathogenicity of a mycobacterium strain.

17. The purified polynucleotide of claim 11, wherein the ORF encodes all or part of a Polymorphism Glycine Rich Sequence (PGRS).

18. The purified polynucleotide of claim 17, which is SEQ ID N0:4.
19. The purified polynucleotide of claim 17, which is selected from the group consisting of :
  - a) a polynucleotide comprising at least 8 consecutive nucleotides the of SEQ ID N0:5 ;
  - b) a polynucleotide having a sequence that is fully complementary to SEQ ID N0:5 ;
  - c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).
- 10 20. A pair of the purified polynucleotides as claimed in claim 10.
21. A *Mycobacterium tuberculosis* strain Rv37 genomic DNA library that has been deposited in the Collection Nationale de Cultures de Microorganismes under accession number I-1945, wherein said genomic DNA library comprises recombinant bacterial artificial chromosome vectors.
- 15 22. A recombinant bacterial artificial chromosome (BAC) vector, which belongs to the genomic DNA library of claim 21.
23. The recombinant BAC vector of claim 22, which is selected from the group consisting of :  
Rv101; Rv102; Rv103; Rv104; Rv105; Rv106; Rv107; Rv108; Rv109; Rv10;  
20 Rv110; Rv111; Rv112; Rv113; Rv114; Rv115; Rv116; Rv117; Rv118; Rv119;  
Rv11; Rv120; Rv121; Rv122; Rv123; Rv124; Rv126; Rv127; Rv128; Rv129;  
Rv130; Rv132; Rv134; Rv135; Rv136; Rv137; Rv138; Rv139; Rv13; Rv140;  
Rv141; Rv142; Rv143; Rv144; Rv145; Rv146; Rv147; Rv148; Rv149; Rv14;  
Rv150; Rv151; Rv152; Rv153; Rv154; Rv155; Rv156; Rv157; Rv159; Rv15;  
25 Rv160; Rv161; Rv162; Rv163; Rv164; Rv165; Rv166; Rv167; Rv169; Rv16;  
Rv170; Rv171; Rv172; Rv173; Rv174; Rv175; Rv176; Rv177; Rv178; Rv179;  
Rv17; Rv180; Rv181; Rv182; Rv183; Rv184; Rv185; Rv186; Rv187; Rv188;  
Rv18; Rv190; Rv191; Rv192; Rv193; Rv194; Rv195; Rv196; Rv19; Rv1; Rv201;  
Rv204; Rv205; Rv207; Rv209; Rv20; Rv214; Rv215; Rv217; Rv218; Rv219;  
30 Rv21; Rv220; Rv221; Rv222; Rv223; Rv224; Rv225; Rv226; Rv227; Rv228;  
Rv229; Rv22; Rv230; Rv231; Rv232; Rv233; Rv234; Rv235; Rv237; Rv240;  
Rv241; Rv243; Rv244; Rv245; Rv246; Rv247; Rv249; Rv24; Rv251; Rv252;  
Rv253; Rv254; Rv255; Rv257; Rv258; Rv259; Rv25; Rv260; Rv261; Rv262;  
Rv263; Rv264; Rv265; Rv266; Rv267; Rv268; Rv269; Rv26; Rv270; Rv271;  
35 Rv272; Rv273; Rv274; Rv275; Rv276; Rv277; Rv278; Rv279; Rv27; Rv280;

Rv281; Rv282; Rv283; Rv284; Rv285; Rv286; Rv287; Rv288; Rv289; Rv28;  
Rv290; Rv291; Rv292; Rv293; Rv294; Rv295; Rv296; Rv29; Rv2; Rv301;  
Rv302; Rv303; Rv304; Rv306; Rv307; Rv308; Rv309; Rv30; Rv310; Rv311;  
Rv312; Rv313; Rv314; Rv315; Rv316; Rv317; Rv318; Rv319; Rv31; Rv32;  
5 Rv322; Rv327; Rv328; Rv329; Rv32; Rv330; Rv331; Rv333; Rv334; Rv335;  
Rv336; Rv337; Rv338; Rv339; Rv33; Rv340; Rv341; Rv343; Rv344; Rv346;  
Rv347; Rv348; Rv349; Rv34; Rv350; Rv351; Rv352; Rv353; Rv354; Rv355;  
Rv356; Rv357; Rv358; Rv359; Rv35; Rv360; Rv361; Rv363; Rv364; Rv365;  
Rv366; Rv367; Rv368; Rv369; Rv36; Rv370; Rv371; Rv373; Rv374; Rv375;  
10 Rv376; Rv377; Rv378; Rv379; Rv37; Rv381; Rv382; Rv383; Rv384; Rv385;  
Rv386; Rv387; Rv388; Rv389; Rv38; Rv390; Rv391; Rv392; Rv393; Rv396;  
Rv39; Rv3; Rv40; Rv412; Rv413; Rv414; Rv415; Rv416; Rv417; Rv418; Rv419;  
Rv41; Rv42; Rv43; Rv44; Rv45; Rv46; Rv47; Rv48; Rv49; Rv4; Rv50; Rv51;  
Rv52; Rv53; Rv54; Rv55; Rv56; Rv57; Rv58; Rv59; Rv5; Rv60; Rv61; Rv62;  
15 Rv63; Rv64; Rv65; Rv66; Rv67; Rv68; Rv69; Rv6; Rv70; Rv71; Rv72; Rv73;  
Rv74; Rv75; Rv76; Rv77; Rv78; Rv79; Rv7; Rv80; Rv81; Rv82; Rv83; Rv84;  
Rv85; Rv86; Rv87; Rv88; Rv89; Rv8; Rv90; Rv91; Rv92; Rv94; Rv95; Rv96  
and Rv9.

24. The recombinant BAC vector of claim 22, which is selected from the  
20 group consisting of :

Rv234; Rv351; Rv166; Rv35; Rv415; Rv404; Rv209; Rv272; Rv30; Rv228;  
Rv233; Rb38; Rv280; Rv177; Rv48; Rv374; Rv151; Rv238; Rv156; Rv92; Rv3;  
Rv403; Rv322; Rv243; Rv330; Rv285; Rv233; Rv219; Rv416; Rv67; Rv222;  
Rv149; Rv279; Rv87; Rv273; Rv266; Rv25; Rv136; Rv414; Rv13; Rv289; Rv60;  
25 Rv104; Rv5; Rv165; Rv215; Rv329; Rv240; Rv19; Rv74; Rv411; Rv167; Rv56;  
Rv80; Rv164; Rv59; Rv313; Rv265; Rv308; Rv220; Rv258; Rv339; Rv121;  
Rv419; Rv418; Rv45; Rv217; Rv134; Rv17; Rv103; Rv21; Rv22; Rv2; Rv270;  
Rv267; Rv174; Rv257; Rv44; Rv71; Rv7; Rv27; Rv191; Rv230; Rv128; Rv407;  
Rv106; Rv39; Rv255; Rv74; Rv355; Rv268; Rv58; Rv173; Rv264; Rv417;  
30 Rv401; Rv144; Rv302; Rv81; Rv163; Rv281; Rv221; Rv420; Rv175; Rv86;  
Rv412; Rv73; Rv269; Rv214; Rv287; Rv42 and Rv143.

25. A *Mycobacterium bovis* BCG strain Pasteur genomic DNA library,  
wherein said genomic DNA library comprises recombinant bacterial artificial  
chromosome vectors.

26. A recombinant bacterial artificial chromosome (BAC) vector, which belongs to the genomic DNA library of claim 25.

27. A recombinant BAC vector according to claim 26, which is selected from the group consisting of :

5 X0001; X0002; X0003; X0004; X0006; X0007; X0008; X0009; X0010; X0012; X0013; X0014; X0015; X0016; X0017; X0018; X0019; X0020; X0021 and X0175.

28. A method for detecting a mycobacterial nucleic acid in a biological sample comprising the steps of :

10 a) contacting the recombinant BAC vector according to claim 22 or 26, or a purified polynucleotide according to claim 10 with the mycobacterial nucleic acid in the biological sample ; and

b) detecting a hybrid nucleic acid molecule formed between said recombinant BAC vector or said purified polynucleotide and the mycobacterial nucleic acid in the biological sample.

15

29. The method of claim 28, further comprising before step a), making the mycobacterial nucleic acid in the biological sample available to a hybridization reaction.

20 30. A method for detecting mycobacterial nucleic acid in a biological sample comprising the steps of :

a) contacting a first polynucleotide according to claim 10 that has been immobilized onto a substrate with the mycobacterial nucleic acid in the biological sample ; and

b) contacting a hybrid nucleic acid molecule formed between said first polynucleotide and the mycobacterial nucleic acid in the biological sample with a second, labeled polynucleotide according to claim 10, wherein said second polynucleotide and said first polynucleotide have non-overlapping sequences.

25

30 31. The method of claim 30, further comprising before step a), making the mycobacterial nucleic acid in the biological sample available to a hybridization reaction.

32. The method of claim 30 or 31, further comprising before step b), removing the mycobacterial nucleic acid that is not hybridized with the immobilized first polynucleotide.

35 33. A method for detecting mycobacterial nucleic acid in a biological sample comprising the steps of :

- a) contacting the mycobacterial nucleic acid in the biological sample with a pair of purified polynucleotides according to claim 20 ;
- b) amplifying said mycobacterial nucleic acid ; and
- c) detecting the amplified mycobacterial nucleic acid.

5 34. The method of claim 33, further comprising before step a), making the mycobacterial nucleic acid in the biological sample available to a hybridization reaction.

35. A kit for detecting a mycobacterium in a biological sample comprising :

10 a) a recombinant BAC vector according to claim 22 or 26, or a purified polynucleotide according to claim 10 ; and

b) reagents necessary to perform a nucleic acid hybridization reaction.

36. A kit for detecting a mycobacterium in a biological sample comprising :

15 a) a recombinant BAC vector according to claim 22 or 26, or a first polynucleotide according to claim 10 that is immobilized onto a substrate ;

b) reagents necessary to perform a nucleic acid hybridization reaction ; and

c) a second polynucleotide according to claim 10, wherein said second polynucleotide is radioactively or non-radioactively labeled, and wherein said 20 second polynucleotide and said first polynucleotide have non-overlapping sequences.

37. A kit for detecting a mycobacterium in a biological sample comprising :

25 a) a pair of purified polynucleotides according to claim 20 ; and

b) reagents necessary to perform a nucleic acid amplification reaction.

38. A method for detecting the presence of a genomic DNA, a cDNA or a mRNA of a mycobacterium in a biological sample, comprising the steps of :

30 a) contacting the biological sample with a plurality of BAC vectors according to claim 22 or 26, or purified polynucleotides according to claim 10 that are immobilized on a substrate ; and

b) detecting the hybrid complexes formed.

39. A kit for detecting a genomic DNA, a cDNA or a mRNA of a mycobacterium in a biological sample, comprising :

35 a) a substrate on which a plurality of BAC vectors according to claim 22 or 26, or purified polynucleotides according to claim 10 have been immobilized.

40. A method for detecting a polynucleotide of mycobacterial origin in a biological sample, said method comprising :

- a) aligning at least one polynucleotide contained in a recombinant BAC vector according to claim 22 or 26 on the surface of a substrate ;
- 5 b) contacting the polynucleotide in the biological sample with the substrate on which the polynucleotide of step a) has been aligned ; and
- c) detecting a hybrid nucleic acid molecule formed between the polynucleotide in the biological sample and the aligned polynucleotide of step a).

41. A kit for detecting a polynucleotide of mycobacterial origin in a biological sample, comprising :

- a) a substrate on which at least one polynucleotide contained in a recombinant BAC vector according to claim 22 or 26 has been aligned.

42. The method of claim 9, wherein the procedure by which the polynucleotide contained in a clone of a BAC DNA library is prepared, further comprises amplifying the polynucleotide insert.

43. The method of claim 9, wherein the procedure by which the polynucleotide contained in a clone of a BAC DNA library is prepared, further comprises digesting the polynucleotide insert with at least one restriction endonuclease.

20 44. The method of claim 42, further comprising digesting the amplified polynucleotide insert with at least one restriction endonuclease.

45. The Polynucleotide of claim 16, wherein the mycobacterium strain is *Mycobacterium tuberculosis*.

25 46. The method of claim 33, wherein the amplified mycobacterial DNA is detected by gel electrophoresis or with a labeled polynucleotide according to claim 10.

47. The kit of claim 37, further comprising a polynucleotide according to claim 10.

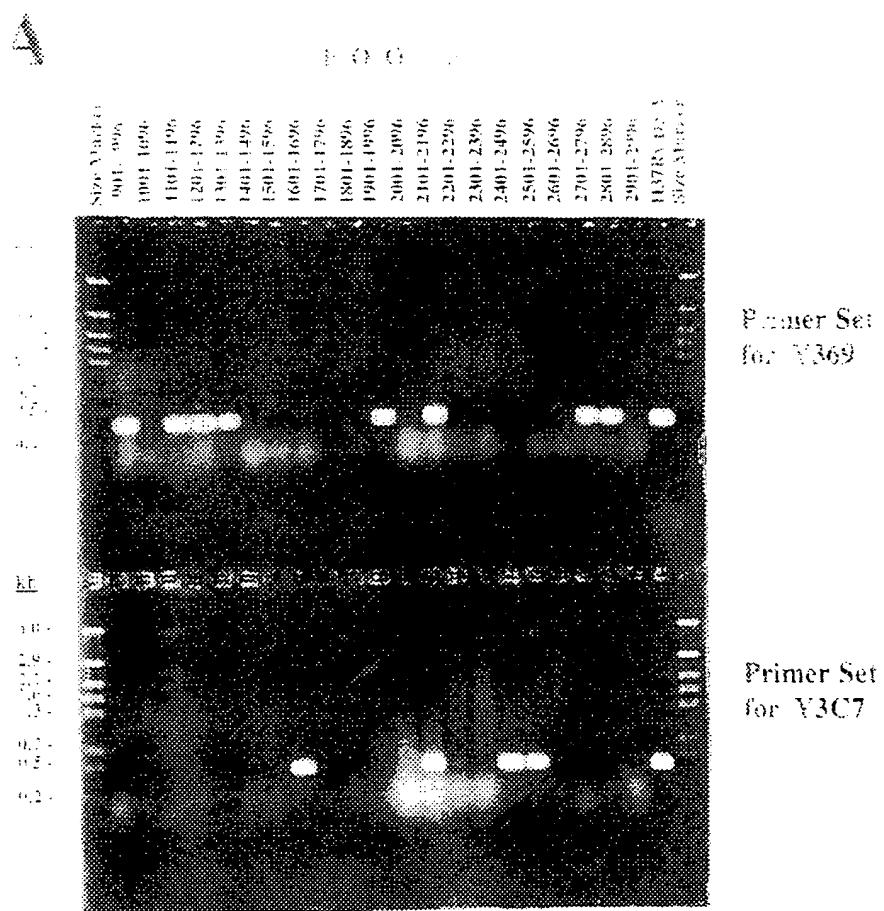
30 48. The kit of claim 39, further comprising reagents necessary to perform a hybridization reaction.

49. A method for physically mapping a polynucleotide of mycobacterial origin in a biological sample, said method comprising:

- a) aligning at least one polynucleotide contained in a recombinant BAC vector according to claim 22 or 26 on the surface of a substrate;

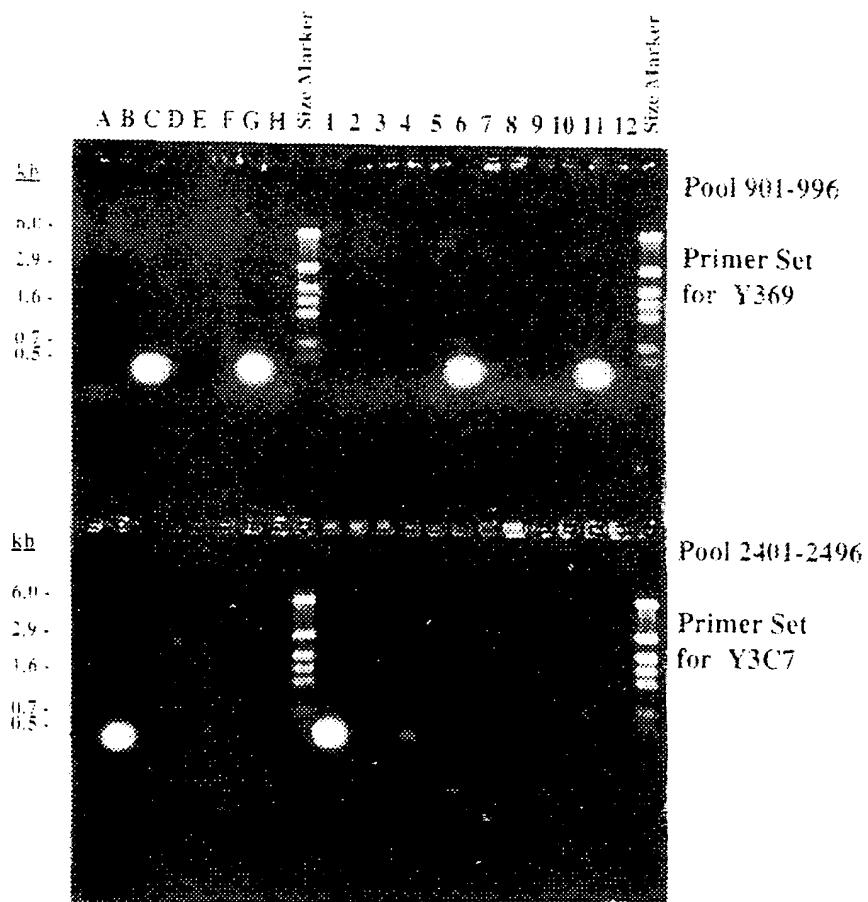
- b) contacting the polynucleotide in the biological sample with the substrate on which the polynucleotide of step a) has been aligned under hybridizing conditions; and
- c) detecting the location of the hybridized polynucleotide from the biological sample.

5. 50. The kit of claim 41, further comprising reagents necessary for labeling DNA and reagents necessary for performing a hybridization reaction.



## FIGURE 1A

**SUBSTITUTE SHEET (RULE 26)**

**B****FIGURE 1B****SUBSTITUTE SHEET (RULE 26)**

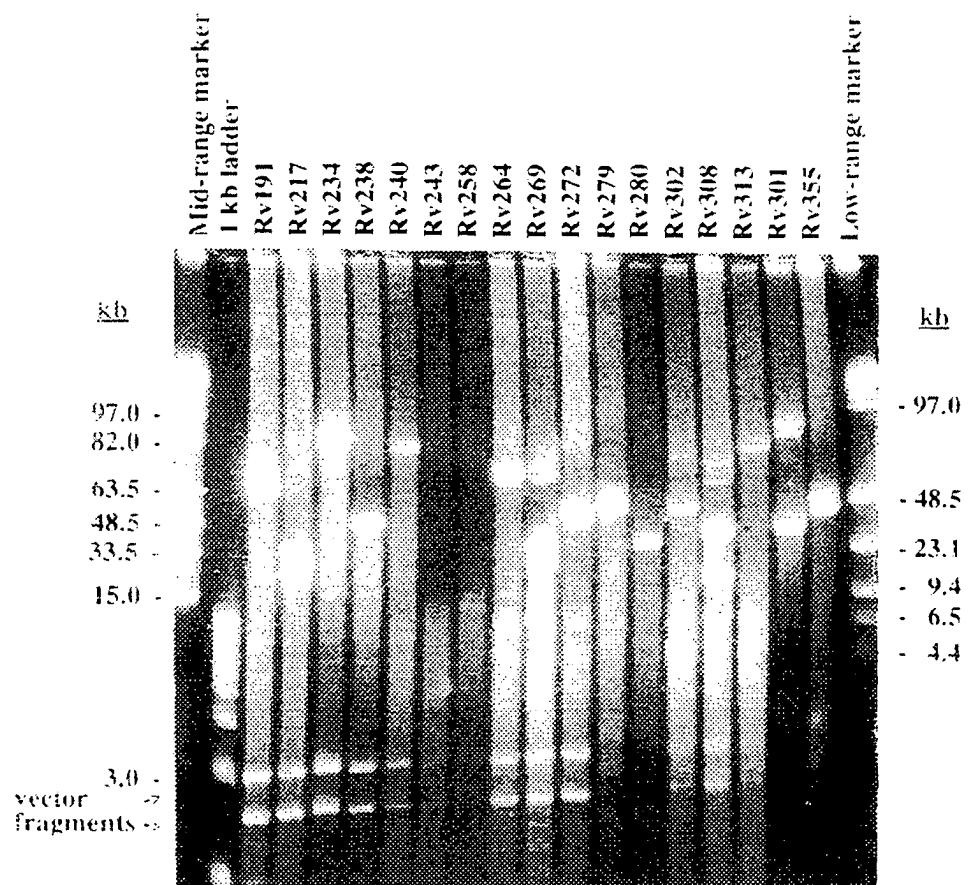
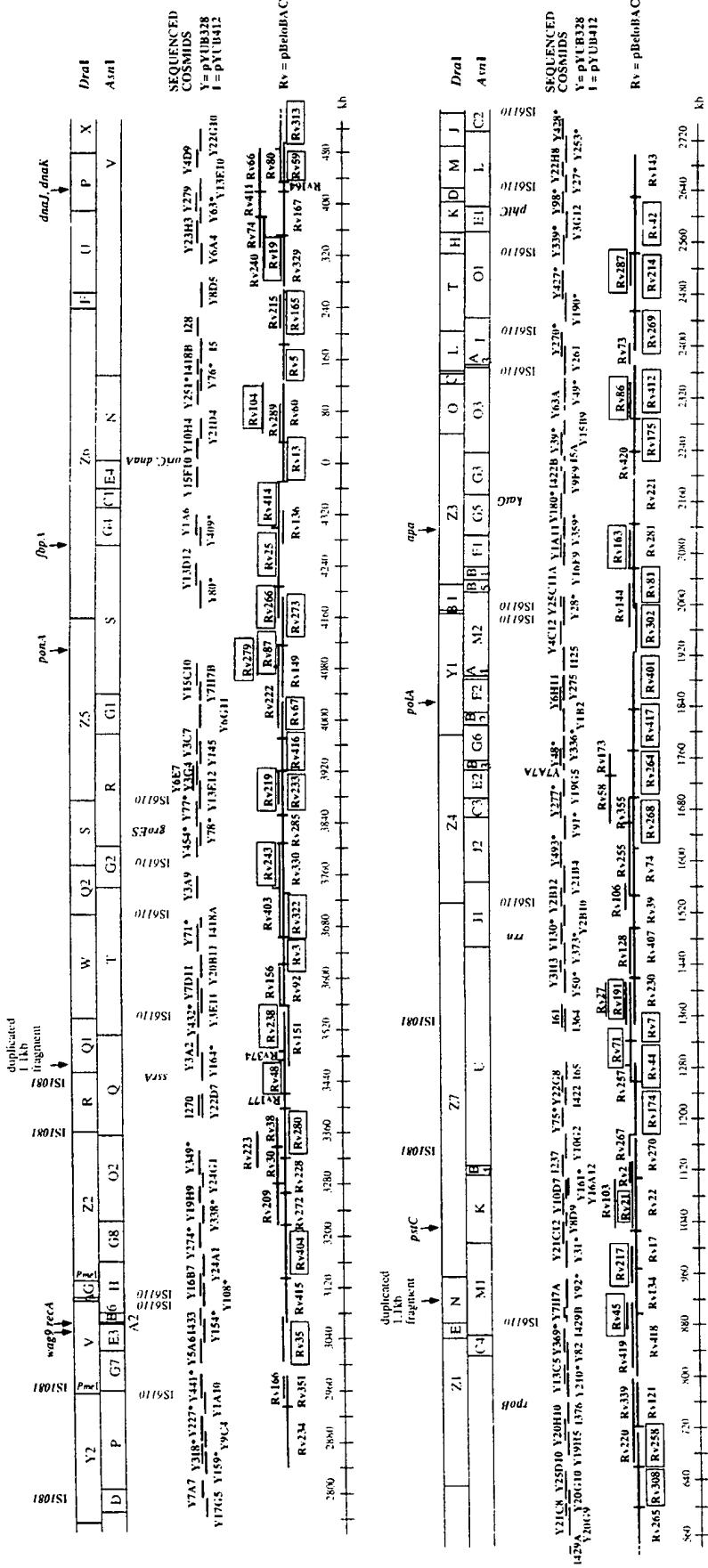
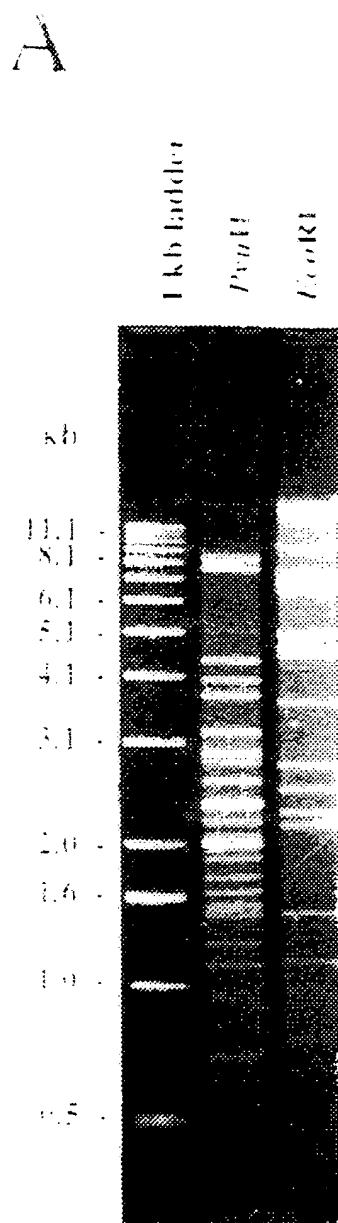


FIGURE 2

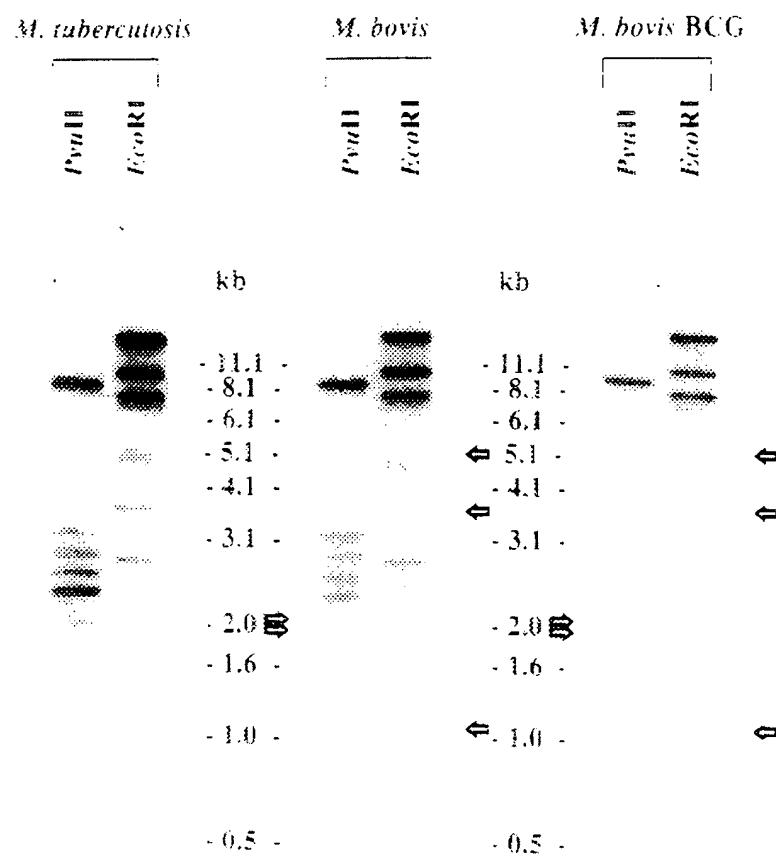
SUBSTITUTE SHEET (RULE 26)



**SUBSTITUTE SHEET (RULE 26)**

**FIGURE 4A****SUBSTITUTE SHEET (RULE 26)**

B



## FIGURE 4B

**SUBSTITUTE SHEET (RULE 26)**

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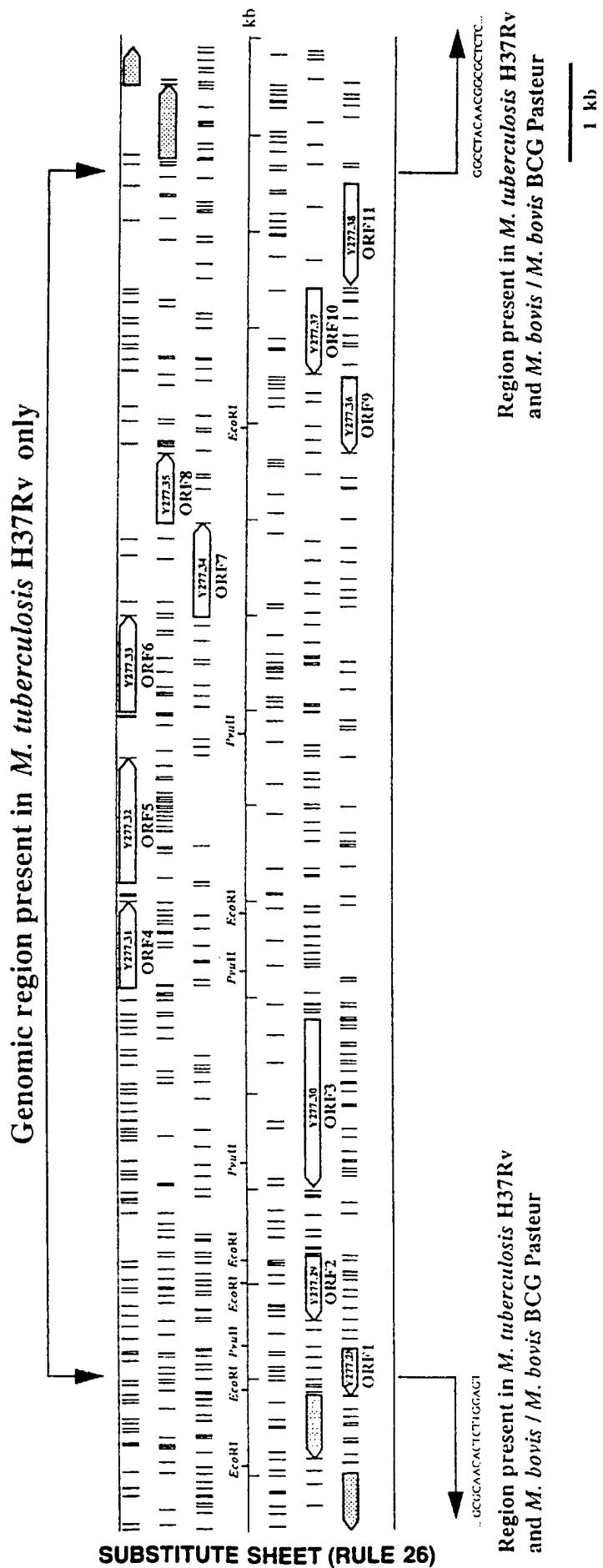


FIGURE 5

**SUBSTITUTE SHEET (RULE 26)**

FIGURE 6

pBeloBAC11

**GGGGCGCG**AA GGGGTCGCG TCAGCGGGTG TTGGCGGGTG TCGGGGCTGG  
*NotI* restriction site

CTTAACATATG CGGCATCAGA GCAGATTGTA CTGAGAGTGC ACCATATGCG

GTGTGAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC ATCAGGCGCC

ATTCGCCATT CAGGCTGCGC AACTGTTGGG AAGGGCGATC GGTGCGGGCC

TCTTCGCTAT TACGCCAGCT GGCGAAAGGG **GGATGTGCTGCAAGGCGATT**  
 primer T7-BAC1

AAGTTGGGTA ACGCCAGGGT TTTCCCAGTC ACGACGTTGT AAAACGACGG

CCAGTGA **ATGTAATAGGAC** TCACTATAGG **GGCGAATT** CGA GCTCGGTACC  
 T7-promoter sequence

CGGGGA **TCCCTAGAGTCGA** CCTGCAGGCA **TGCAAGCTTG** AGTATTCTAT  
 primer T7-Belo2 **HindIII cloning site** SP6-promoter

**AGTGTGACCT** AAAATAG **CTTG** GCGTAATCATGGTCATAGGTG **GTTT** CCTGTG  
 sequence (complementary strand) primer SP6-Mid (complementary strand)

TGAAATTGTT ATCCGCTCAC AATTCCACAC AACATACGAG CCGGAAGCAT

AAAGTGTAAA GCCTGGG **TG** CCTAATGAGT GAGCTAAC **TG** ACATTAATTG  
 primer SP6-BAC1 (complementary strand)

CGTTGCGCTC ACTGCCGCT TTCCAGTCGG GAAACCTGTC GTGCCAGCTG

CATTAATGAA TCGGCCAACG CGAACCCCTT **GGGGCGCG**CC GGGCCGTG  
*NotI* restriction site

FIGURE 7

SUBSTITUTE SHEET (RULE 26)

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

- (A) NAME: INSTITUT PASTEUR
- (B) STREET: 28 RUE DU DOCTEUR ROUX
- (C) CITY: PARIS CEDEX 15
- (E) COUNTRY: FRANCE
- (F) POSTAL CODE (ZIP): 75724

(ii) TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA LIBRARY. APPLICATION TO THE DETECTION OF MYCOBACTERIA.

(iii) NUMBER OF SEQUENCES: 5

## (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12732 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ACCTGCGCTT GCAGAGATCA AATAGGGCGC ATGGGTAGC ATAGTACAGG TCGTCGCGCA	60
TCTTGATGC ATCGGAATAA GATGTCAGGC ATTAAAAGA GAAGCCACGG CGACTCGCGG	120
CATTCAGCAT GTCGAGCGTC GCTTCGATGT GAGCGCACCA TTCCGTGTCC AACGATTCA	180
GACGAACATT GAATATTCCA CTCGCGACGC TATAGTCCGC CTCCCGATCT ATGCGCGCCG	240
CGCAGATGAA GTCTGCGTTC GCCCGACCTT CGAAACGTAG TGCGGCCGCG CGCACCAATT	300
CGGGGGAGAC GTCGATGCCG GTGTAATCAG TTTTGAAGCC ACGCGCATCT AGGTAGTCCA	360
GTAGAGCCCC ATAGCCACAG CCTAGATCGT TGATCGAAAA TGGGTCCGCC GCATTGACAA	420
TGCGCACCAG CTGGTCAAAG CGCAACGCCT GCCCGGCTTC GCCGTTCAA TCGACGCCGC	480
GCGGGTGCCG TGTGCTTCGA GTTCGATGC GTAGTAACGG GCCACGTCAG CGAGCATGGT	540

CGTTGCGTCT	TCCGCCATGA	AGCTGCCCTCA	CGATTTGTGT	GTGTGGGCGT	CGGTGCGTGG	600
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CCCGCCGGCA	CGGTTCGCCG	AGCAAGGAAG	CGTGGAGACG	ATAGATAATT	TCACTGGCGA	720
CAGTACCTCA	AATAGTCCGG	AGCCTCGGCT	CCGACGTTAA	AGAGCAGATC	CAGAATCGAC	780
ACGGCGGGCT	CGAACCCCTCC	CCACAATTGC	TTATAATCGC	GGTAGCCGTC	ATAATCGAAC	840
CAAGTTACCC	GGATGCTAAG	TTCGTCGAAC	ACGCGCTCAT	CGACATACGA	ACGGGCTGAG	900
GGGCCAGAGA	CATATTCGGT	CGCTGCGGCC	TGTTGGCAGA	GGTTGCCAG	TCTCTCGGTC	960
TTGCCGTCGG	CTAATTCTGA	GTCCCACGAA	TTGCCAGTC	CGTGCTGAT	ACCGAGATAA	1020
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AGGTAAATCG	GCGCGAGCCA	GTCAGCGATC	TCCGCAAAAT	GAGCGGCCGC	GCTGTAGTTG	1140
AATTCTAGTG	CCCGCCAGTG	CGCTTCGCC	CAATCGGTGC	CGTCGATCAG	CGTCTCACGT	1200
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GCTCGGGAAG	GCCAGGATGG	GCCGCGACCC	GGGGCGTCCG	GTGCGCGATG	AACGTCGCAT	1560
CGTCTCCTGT	GAGATAATTG	CATCCGATCA	TATAGGGCTG	GCTGCGCTA	GGTTGCTGGC	1620
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TCACGAGATC	GATTCCCTGGT	CTTCCCCCAG	CGTCGCGATG	TCGATAGGTG	TCGCGCTTTG	1740
TTCGTACCCG	CACTACGCGG	CGGCGAGAAC	CTCGCCACCG	AATCGGGATT	GGGGGGAGGA	1800
TACCACTCGG	TCGAGGCCCG	TCACCGGCCT	TCTAGCGGGT	TGACCATCAG	TGTTTGCAGG	1860
GCCCTATCCC	GGTATGGCGC	ACCACGGGAT	CGGCAGCGTT	CCGGTTGCTG	GCGTGGTACC	1920
TCGTTGTGGC	GCCGTGGTCC	ATGTCGATTG	AGTGCCTGGA	TCAGTGTAAA	CCGTTGCGCG	1980
CCATGTTCTG	TAGGCACTGG	TTCGGTTGT	GGTTAGGCTG	CACGGTTGGC	AGGTTACCAA	2040
CCACTGAGCC	CCTGGGCCGA	TGTGAGCTCG	GACTCCGCCT	ATGGGGTGT	ATTTTGGCAG	2100
ATTGGGCCGG	GTCCCCGTGG	TGAGGACTCC	TCAACCGGAT	TGGGTAAGCA	TGAGGTGGTG	2160
CTGGCAGCGG	TGTCCCTGGC	GCTCTCCCGA	GTAGGCCCGT	TGTGACTGTC	ATGTGGCGA	2220

GC GG GTT GC GCG GTAGGA GAC GAT GATT ACT ACG CAC G TG ACC AAC CA CA AGAAC CG GT	2280
GCC CAT GTCA CCG TGG TGAA AAC GAG TGG C GT GGT ACC GA CT ACC CTT TT GG CT CCC AGC	2340
TGT CCAT AGA GCG GCAC GTGA GAA CGG CT GG CCC CGG AAC CG CG AC GTT GAC GAT GCT CAG C	2400
GCC AC GG CC CA AAC T CAC GCA GAC GCG GAC C GCG CGG CGG C GGT CT CC ATG GG CT GCG AGT	2460
TGG TCG AATA TCCC AGC ACC AGG AGG CCG TT GGG GTCT C GGG CT ACC AG TGC AGC GATT	2520
GG CA AGA CGA AA AC GAG A TA GT AGA AGG CG AC GT CC GCG G GGG AGA AGG T GG CG GT GG CG	2580
AG CA AC AC AA TCCC ACC AT GAC AGG CGG AT AC GG CG TC CG AGC GCC AG CAC GG CG ACC	2640
AC GACT AT GA CT AGG AC AGC AA ACC CG ATC TGC GTT CG CG GAC CAG TGAG GAA ACC CT CT	2700
GGG AT CT TG C CCG ATT GATA GT TCT TGAT G CT AT CGG GGA TC AGC AGG AG TGC CT TGCCA	2760
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AA AC ACC AC GC CG AGA AC GAC GAA CT GCG GC TTT ACC AGG A CGG CCA AG AT CAC CGT GAT G	3000
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CC CAG CCA AT GG CT GG GT AG TCC GAA ATC GCA TAC CGT A TG CGG CG GGG GG CC AT GCA	3300
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GCT A AG CT CC CG CT GA AG GGG AT AT GT GG CC GCT GG TA GCG CC GAG GT CT AT TT CT GCG	3960

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CACCCACGGC	CTCCTGCAAG	AAACGACCCG	CGAGGTCCGC	TGGGTGCGCT	CCACCCAAAT	5580
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CGCGCGCAGC	CGGGCCAGCC	TGCTGACGCC	CGGGGAAATC	GCCACGTTCG	TGCGCGGTGC	6000
CGCTCATTG	ATAACCGCCG	CGGGTGCCAG	CGCGATTCTG	GTAATGGTT	TCCCAGTGT	6060
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TTTCGTCGAC	CGGCGCACCC	AACGGCTTCG	GGCGCTGATC	GCACCGGCGC	TGGTCGTCGG	6240
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GGTAGCTATC	GCCATGCTGA	CGCTGACCGG	CGCCGCCGCG	GTCGCGGCCG	CACTGCACCG	6420
GGCGTATTTG	CTGGGCTGGG	TCAGCGCGAC	GGTGGCGTCG	ACGCTGTTGC	TGCTGCTGCC	6480
GATGCCGCTG	GAGACGCGCA	CCGTGATCGC	GCTGTTGTT	GGTCCAACGG	TGGAATCGC	6540
CATCCATGTG	GCCGCGTTGG	CGCGCGACCC	CGACTGATTT	GTGCCCCAGG	TCGACAAATC	6600
ACGCCGTCTC	GTCAGTGAGC	ACTCCGTCT	CGGGTCCGAT	CCTTCCAGGA	GACGTTGCAA	6660
CCTGATTTGG	CTCAAATTGG	TGCGCACCGA	GGGTGGGCA	CATCGTAGGG	TCGCAACAGT	6720
CACATGTGTC	ACTGCACCGG	GCGACACCCG	ATGTCCCAGG	TCTCAGCGAC	AGCTGTCTGA	6780
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GCGTCGTATG	GATTCTCCTC	CTCGGTTCCG	CGCGAACCGG	CCGCAGGCGC	AATGGTCACC	6900
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AATCACCGGC	CAGGACGGCT	CGTATCTCGC	CGAACTGCTG	CTGGCCAAGG	GGTATGAGGT	7140
TCACGGGCTC	ATCCGGCGCG	CTTCGACGTT	CAACACCTCG	CGGATCGATC	ACCTCTACGT	7200
CGACCCGCAC	CAACCGGGCG	CGCGGCTGTT	TCTGCACTAT	GGTGACCTGA	TCGACGGAAC	7260
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CCCGCGGTCA	CCGTATGGCG	CCGCCAAGGT	CTATTCGTAC	TGGGCGACCC	GCAATTATCG	7560
CGAACCGTAC	GGATTGTTCG	CCGTTAACGG	CATCTTGTTC	AATCACGAAT	CACCGCGGCG	7620
CGGTGAGACG	TTCGTGACCC	GAAAGATCAC	CAGGGCCGTG	GCACGCATCA	AGGCCGGTAT	7680
CCAGTCGAG	GTCTATATGG	GCAATCTGGA	TGCGGTCCGC	GAECTGGGGT	ACCGCGCCGA	7740
ATACGTCGAA	GGCATGTGGC	GGATGCTGCA	GACCGACGAG	CCCGACGACT	TCGTTTTGGC	7800
GACCGGGCGC	GGTTTCACCG	TGCGTGAGTT	CGCGCGGGCC	GCGTTCGAGC	ATGCCGGTTT	7860
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GGCGATGAAG GTCGCCCATG CGGCGCAGAT CACCGAAGAC CGCGTTGGT TCCCGGTGCG	9960
AGCCGACGCC CGTGGTGTG AACTCGCACA GCACACACCG AATCGTGACC GGCTCGCATA	10020
CCAGCGCGGC CCGCAATATG AATTCTGGT CGGCGCGCAT CCCGAAATCA AGGTCGTAGC	10080
CACCGATCTT GGCCACCAGC GATGATCCGA AGAACGATGC TTGATGCGGA ACAACCTGCT	10140
TGCCGCCAG GAATTTGCGC AGGCTGAAAG GTATCGGGCC GCGCACCCGA TCGAGCCCGA	10200
CGAGACGATC CATCCGAAG CCCCACAATT CGGACACCCGG TCCCTGCCG GATAGCGCCT	10260
CCACGGCCTG GGCTACCACG TCGGGCCCGG AAAAACGATC GGCGGAGTGC AAGAACACAA	10320
ACAGATCACC CGATGCGTGC GCGATGCCCT GGTTCATCGC GTCGTACCGC CCGCCGTCGG	10380
GCTCGGACTG CCAATACGCG AAGCCTGGTT CACACCCGGA CAGGTATGCC ACCACGTCGT	10440
CGCCGCTGCC ACCGTCGATT ACGATGTGCT CGATGCGTCC CGGGTAGCGT TGCGCCCGCA	10500
CACTTTCAC CGTGCCTGC AACCCGTCGA GGTCGTTGAA CGAGATCGTT ATCACCGAGA	10560
CGGTCGGAGC AGACGTCACC GAGTTCCCT AGGTTGCTGG CGGCATGTT GGATCACCGG	10620
GTCTTGATAC CGATGAAGGT GCCTCGAAGA TTGCGCGCAT AGGAACCTCC GAGCAACGAC	10680
TCGGCGATGC TTGGTTCCAA GTTGTGTCAC TCCTCCATCA CCAGGTCGAC GCCGACGTCT	10740
TTGATGGCCT GAAGTAGGTG CTCGCGTTGA ATCCAGAACATG ACCGGCGATT GTCCCAGGAC	10800

GCCCATTTG	CGGTGTCGCG	CTGGCCAAAC	GAGCGGTCGT	CGGAAAACTC	GGTAAACCAC	10860
CTACCGGGAA	GTCCCTCATG	TTCGGTGGC	GCCGAGAGCA	TGAACCTCAC	CGGCGCCGGC	10920
CGCCGCAGCA	ACCGATCGGT	CAATTGTCGT	GCCGTCGTGG	GCAACCGGAG	CCATTTATCG	10980
CTCCGGTTGA	TGATCGAGAA	GTGCGTCTGG	AGAACATCAGCA	GCTTGTTCGT	TACCGACGAG	11040
AGGGTTTCCA	GGTATTGCTT	CGGATTCTCC	AGGTGGTAGA	AGAGGCCGCA	GCAGAAAGACG	11100
GTATCGAAGA	GCCCCGTGGTT	GGCGATGTTG	AGGGCGTTGT	CGTGGACGAA	CCGGAGATTC	11160
GGCAGGTTGG	TCTTCGATTT	GATGTAGTTG	CAGGCCGCCA	TGTTCAGCTC	GCGAACCTCG	11220
ATCCCGAGGA	CCTGAAATCC	CATGCGCGCG	AACCCGACCG	CGTACCCGCC	TTCCAAGCAG	11280
CCGACATCGG	CCAGGCGTAG	GTGGCTCTTG	TCCCCGGGAA	AGACGGTTTC	CAGAATCCCG	11340
CGCGCCGAGA	TGAACCAGGA	CGATTGTCGT	AACGTGCGCG	AGGACTCCGG	TATCGTCAAG	11400
GTTCCGTCGT	CGAGGCGAAC	GTTGTGGCG	GTGAATTGTA	CCGCGCCGGC	CGAATGTTCC	11460
TGTGCCATCA	CTTGGTTAGC	CCCTTCGGCT	GGTCCTGGGT	TTGTCGACAT	GGTCAGGCTC	11520
GACAGCCGCG	TCGGAGCCGG	GAGGCCACA	CATCCACGAG	CCCCCTGCCG	CTCGCGTCG	11580
CGGCGGCGAG	CTTGCGCCAC	TGGGTCTTGA	GCCGCCGCGC	GGGTGTCGCC	CCGCGGTGCT	11640
GCAGCGCCAG	CATGGCGATC	CGGGGATGGC	GCGCGATGGT	TTCCTGCAGC	GCGGCGCGCC	11700
CCTCCGGGCC	TGGAACGTTG	GCGATCTGGC	GAAGGATCCA	GTCGGCCATG	ACGGCGATGA	11760
GCTCCTCGCG	CGCGGGGTCT	CCCGGAACA	GGTCGAGCAT	CGCGTCAAAC	GTCGCCGCAT	11820
GCCCCGGACC	CTGCGTCAAC	CAGAACTTTG	GCGGGTCCAC	CACCTGGTTG	TGCCACATGC	11880
CTTGGCGTG	GCGCGATAC	ACGGCCATGG	TGTCGGCAA	CATGGCGATG	TCGCCATGCA	11940
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CATCCAGGCT	CAAGTTGCC	CGCACCCGAA	CCGGGGGGAA	CTTCGAGTCC	TTGGCATGGC	12120
CGTCCTCCCA	TATCACTCGG	ACGGGATGGA	AGCACACCGT	CGTCTTGGGG	TGCCGGTCGA	12180
GGAATGCGAC	CTGTTTGCTT	AGCTTCAGCG	GATCGATCCA	GTAGTCGTCC	GCCTCGCACA	12240
ACGCGACGTA	CTCGCCGCGA	GCGGCCGACA	GGGCGCCGGT	CAGGTTCCCA	TTGAGGCCGA	12300
GGTTTTCGGT	CCTGAAGATC	GGCCGGAACA	CGTGCAGGTA	CCGCTCGGCCG	TACTCACGGA	12360
TGATCGCCGG	GGTGGCATCG	GTCGACGCGT	CGTCGGCGAC	GATGATCTCC	ACCGGGAAAGT	12420
CGGTTTGCTG	GTCGAGAAAG	CTGTCGAAGG	CCTGACGGGC	GTAGCCCGCC	TGTTGTGAG	12480

TGGTCGAGAC GATGCTCAC	TTGGGGCAAA GCTGGGGACT CACCGTCGGC CCTTTTCCTG	12540
CGCGGCCGCA AGGGTATTGC GATGGCGAAC GTGAATCGCC TGTGCCCGCC GGCGTCGGC	12600	
CGTCGTGGCC TGGTGGTCGG CGGACGTACG GCACACGCTG GCGAAGTATA GCGAGGGTGC	12660	
ACTGACGTTG GGCTCGAAC	CCGTGGCGCG CGGTGTGGC GCACCGTCTC GAGTCGGTGC	12720
TGGTTGGCTC GC		12732

## (2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 289 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATACTCAAGC TTGCCGCAAT CGAAACCAAC CTGTTTGTGC CGCAAGAAAT TACGCCGTGG	60
CCCGCGCCG ATCAAGAAAC GCCCCGGCGC GCGGCGGTGT CGTCGTATGG CATGACGGC	120
ACCAATGTGC ACGCCATTGT CGAGCAGGCA CCGGTGCCAG CCCCCGAATC CGGTGCACCA	180
GGCGACACCC CGGCCACACC CGGTATCGAC GGCGCGCTGC TGTCGCGCT GTCGGCCAGC	240
TCGCAGGACG CGCTGCGGCA AACCGCCGCG CGGCTGGCCG ATTGGGTCT	289

## (2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 278 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TTGGCGGGTT GGCCACACAC CCGCCGGTGA CGGCGACGAT GCTGGGCTGG TTGCGGCCCT	60
GCGCCACCGC GGCTTGCATG CTGGTTGGCT GTCTTGGAC GATCCCGAAA TAGTCCACGC	120
GGATCTGGTG ATTTTGCAGG CTACCCGCGA TTACCCCGCG CGGCTCGACG AGTTTTGGC	180

CTGGACTACC CGCGTGGCCA ATCTGCTGAA CTCGCGGCCG GTGGTGGCCT GGAATGTCCA	240
CGCCGTTCAC CTACGTGACC TTGATGGGAT CCGGGGGT	278

## (2) INFORMATION FOR SEQ ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CCGACCCAGA CACTGACCGG GCGACCGCTG ATCGGCAACG GCACCCCCGG GGCGGTCGGC	60
AGCGGGGCCA CCGGGGCCCG CGGTGGGTGG CTGCTCGGCG ACGGCGGGC CGGCGGGTCC	120
GGCGCGGCCG GCTCGGGCGC GCCCGGCGGG GCGGGCGGGG CTGCCGGCT GTGGGGTACC	180
GGCGGGGCCG GCGGGATCGG CGGAGCCAGC ACCGTACTCG GCGGCACCGG CGGGGGAGGC	240
GGGGTCTGGTG GGCTGTGGGG CGCCGGTGGG GCCGGCGGGG CCGGTGGAAC CGGCCTTGT	300
GGTGGCGACG GCAGGGGCCGG TGGGGCCGGC GGGACCGGCG GACTGCTGGC CGGGCTGATC	360
GGTGCAGCG GAGGTCACGG CGGGACCGGC GGGCTCAGCA CTAATGGCGA CGGCAGGGTT	420
GGCGGGGCCG GCGGGAATGC CGGAATGCTC GCCGGGCCGG GCGGCGCCGG CGGAGCCGGC	480
GGTACGGCG AAAACCTGGA CACCGGTGGG GACGGCGGGG CCGGCGGTAG CGCAGGGCTG	540
CTGTTCTGGCA GCGGCGGCCG CGGCGGCCGC GGCAGGATTTG GTTCTCTCGG TGGGGACGGC	600
GGGGCCGGTG GCAACGCCGG GCTGCTGTTG TCCAGCGCG GGGCCGGCGG GTTCGGCGGG	660
TTCGGCACCG CCGGTGGGGT CGGTGGGCC GGCAGGAATG CCGGCTGGCT GGGCTTCGGC	720
GGGGCCGGGG GCATCGGCCGG AATCGCGGT AACGCTAACG GGGCGCCGG TGGGAACGGC	780
GGCACCGCG GTCAGTTATG GGGTAGCGGC GGCGCCGGCG TCGAAGGCAG CGCAGCCTTA	840
AGCGTCGGCG ACACCGCGG GGCGGGTGGC GTCGCGGCCA GCGCCGGCT GATCGGCACC	900
GGCGGCAACG GCGGCAACGG CGGCACCGGC GCCAACGCCG GCAGCCCCGG AACCGGCCGC	960
GCCGGCGGGT TGCTGCTGGG CCAAAACGGG CTCAACGGGT TGCCGTAGCC GGGCGGCACG	1020
GCATGGCTTC CGGGCGTCAA CCACTCGCCG GTGATGCAGA TCGGCTGCC AGCGGGCCGC	1080

CAAAATGGGG	GCCGCCGCGC	CAGGTATCTC	GGCGAAGATC	CCC GGCGCTC	GAGCGCTTTG	1140
TCAGAGGCC	TCGCGGGTC	GTCGTGACGA	CGGCTATCCG	GGCGGTGCGG	GTTTCGCGGC	1200
GCGCCCTGTG	CCCGGCACCG	CCGCCCGTTT	GTCGGCAACG	CCGCCGCGAC	CCGTGAGCCG	1260
TCCAGCAGCT	GGCGCCTGCG					1280

## (2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GGGCATCGGC	GGAATCGGCG	GTAACGCTAA	CGGGGGCGCC	GGTGGGAACG	GCGGCACCGG	60
CGGTCAGTTA	TGGGGTAGCG	GCGGCGCCGG	CGTCGAAGGC	GGCGCAGCCT	TAAGCGTCGG	120
CGACACC						127



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification <sup>6</sup> :  C12N 15/70, C12Q 1/68		A3	(11) International Publication Number: <b>WO 99/54487</b>  (43) International Publication Date: 28 October 1999 (28.10.99)
(21) International Application Number: PCT/IB99/00740  (22) International Filing Date: 16 April 1999 (16.04.99)		(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).	
(30) Priority Data: 09/060,756 16 April 1998 (16.04.98) US		(Published) <i>With international search report. Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i>	
(71) Applicant (for all designated States except US): INSTITUT PASTEUR [FR/FR]; 28, rue du Docteur Roux, F-75015 Paris (FR).		(88) Date of publication of the international search report: 9 December 1999 (09.12.99)	
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(74) Agents: MARTIN, Jean-Jacques et al.; Cabinet Regimbeau, 26, avenue Kléber, F-75116 Paris (FR).			
(54) Title: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA LIBRARY. APPLICATION TO THE DETECTION OF MYCOBACTERIA			
(57) Abstract  The present invention is directed to a method for isolating a polynucleotide of interest that is present or is expressed in a genome of a first mycobacterium strain and that is absent or altered in a genome of a second mycobacterium strain which is different from the first mycobacterium strain using a bacterial artificial chromosome (BAC) vector. The invention further relates to a polynucleotide isolated by this method and recombinant BAC vector used in this method. In addition the present invention comprises method and kit for detecting the presence of a mycobacteria in a biological sample.			

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## INTERNATIONAL SEARCH REPORT

International Application No

IB 99/00740

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/70 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>PHILIPP W.J. ET AL.,: "Physical mapping of mycobacterium bovis BCG pasteur reveals differences from the genome map of mycobacterium tuberculosis H37Rv and from M. bovis"  <i>MICROBIOLOGY</i>,  vol. 142, - 1996 pages 3135-3145,  XP002118720  cited in the application  the whole document</p> <p>---</p> <p>-/-</p>	1-50

 Further documents are listed in the continuation of box C. Patent family members are listed in annex.

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- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

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Date of the actual completion of the international search

Date of mailing of the international search report

14 October 1999

27/10/1999

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Authorized officer

Müller, F

## INT'L NATIONAL SEARCH REPORT

International Application No

IB 99/00740

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	KIM U -J ET AL: "Construction and characterization of a human bacterial artificial chromosome library" GENOMICS, vol. 34, 1 June 1996 (1996-06-01), pages 213-218, XP002081197 ISSN: 0888-7543 cited in the application the whole document ---	1-50
A	WO 93 03187 A (AMOCO CORP) 18 February 1993 (1993-02-18) see whole doc. esp. claims ---	1-50
A	WO 93 18186 A (UNIV CALIFORNIA) 16 September 1993 (1993-09-16) see whole doc. esp. claims ---	1-50
P,X	BROSCH R. ET AL.: "use of a mycobacterium tuberculosis H37Rv bacterial artificial chromosome library for genome mapping sequencing, and comparative genomics" INFECTION AND IMMUNITY, vol. 66, no. 5, - May 1998 (1998-05) pages 2221-2229, XP002104659 the whole document ---	1-50
P,A	COLE S T ET AL: "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence" NATURE, vol. 393, 11 June 1998 (1998-06-11), pages 537-544, XP002087941 ISSN: 0028-0836 the whole document -----	1-50

## INTERNATIONAL SEARCH REPORT

Information on patent family members

National Application No

/IB 99/00740

Patent document cited in search report	Publication date	Patent family member(s)		Publication date
WO 9303187	A 18-02-1993	EP	0554437 A	11-08-1993
		JP	6502082 T	10-03-1994
		US	5648481 A	15-07-1997
WO 9318186	A 16-09-1993	CA	2131543 A	16-09-1993
		EP	0631635 A	04-01-1995
		JP	7505053 T	08-06-1995
		US	5665549 A	09-09-1997
		US	5721098 A	24-02-1998
		US	5856097 A	05-01-1999